



TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOM									
Qy	181	ATQARPPPHASGPRRLGCEAWNHSVREAGYPLGLPAGARRGSSAERSLPLPKPRRR	240						
Db	181	ATQARPPPHASGPRRLGCEAWNHSVREAGYPLGLPAGARRGSSAERSLPLPKPRRR	240						
Qy	241	GAAPPEBERTPYQGSSIAHPGTRGPDRGFCVSVSPARAEATSLLEGALSTRHSPSVG	300						
Db	241	GAAPPEBERTPYQGSSIAHPGTRGPDRGFCVSVSPARAEATSLLEGALSTRHSPSVG	300						
Qy	301	RQHHAGGPPSTSRPWRPDTPCPVVAETKHPYSSGDKEOLRPSFLSLSPSLTGARL	360						
Db	301	RQHHAGGPPSTSRPWRPDTPCPVVAETKHPYSSGDKEOLRPSFLSLSPSLTGARL	360						
Qy	361	VETIFLGSRPMPGTPLRPLPQRYWQMRPLFELIGHAQCPCYGVLKTHCPURAATV	420						
Db	361	VETIFLGSRPMPGTPLRPLPQRYWQMRPLFELIGHAQCPCYGVLKTHCPURAATV	420						
Qy	421	PAAGYCAREKPGQSYAAPEEEDTPPLVQLRQHSSPQVYGVYRACJERLVPFGLWGS	480						
Db	421	PAAGYCAREKPGQSYAAPEEEDTPPLVQLRQHSSPQVYGVYRACJERLVPFGLWGS	480						
Qy	481	RHNEERFLRNTKFKFSLGKHAKLSQLELTWMRSDCAWLRSPGVGCVPAAEHRLREB1	540						
Db	481	RHNEERFLRNTKFKFSLGKHAKLSQLELTWMRSDCAWLRSPGVGCVPAAEHRLREB1	540						
Qy	541	LAKEFLHMLMSVYVYELLRSFYYTETTEFKQNRLLFFYRKSYWKLQSIGIROLHLKRVOLR	600						
Db	541	LAKEFLHMLMSVYVYELLRSFYYTETTEFKQNRLLFFYRKSYWKLQSIGIROLHLKRVOLR	600						
Qy	601	LSEAEVROREARPAALLTSLRF1PKPDGIRP1VMDVYGVARFRREGRAERLTSRVA	660						
Db	601	LSEAEVROREARPAALLTSLRF1PKPDGIRP1VMDVYGVARFRREGRAERLTSRVA	660						
Qy	661	LFSVLNAYERARRPGLGASVYLGLDDIHRARWTFVLRVRAODPPELYFTVVDTGAYDT1	720						
Db	661	LFSVLNAYERARRPGLGASVYLGLDDIHRARWTFVLRVRAODPPELYFTVVDTGAYDT1	720						
Qy	721	PQDRLTTEVATSIKPQNTYCVRRAVYQKAAGHGYRKFKSYHSTLTDLQPYMQRQFVAHL	780						
Db	721	PQDRLTTEVATSIKPQNTYCVRRAVYQKAAGHGYRKFKSYHSTLTDLQPYMQRQFVAHL	780						
Qy	781	QETSPLRDAVVIQESSLNEASSGLFDVFLREMCHAVAIRGSKSYVQCGCIPQCSILST1	840						
Db	781	QETSPLRDAVVIQESSLNEASSGLFDVFLREMCHAVAIRGSKSYVQCGCIPQCSILST1	840						
Qy	841	LCSLCYGMENKLPGIRRDGLLRLVDFLRFMCHAVIRGSKSYVQCGCIPQCSILST1	900						
Db	841	LCSLCYGMENKLPGIRRDGLLRLVDFLRFMCHAVIRGSKSYVQCGCIPQCSILST1	900						
Qy	901	RKTVVNFNPDEALGGTAVQMPAHLFWFCGGLLDTTRLEVOSDYSSYARTSTRASLT	960						
Db	901	RKTVVNFNPDEALGGTAVQMPAHLFWFCGGLLDTTRLEVOSDYSSYARTSTRASLT	960						
Qy	961	NRGEFKAGRMNMRKLFVGVLRLKCHSFLDQIQLVNSLQTYCNYKILLQAYRPHACVLOLP	1020						
Db	961	NRGEFKAGRMNMRKLFVGVLRLKCHSFLDQIQLVNSLQTYCNYKILLQAYRPHACVLOLP	1020						
Qy	1021	FHQQWKNPTEFLRVRISDASLCLCYSLIKAKNAGMSLGAKGAAGPLPSAVQNLQHAFL	1080						
Db	1021	FHQQWKNPTEFLRVRISDASLCLCYSLIKAKNAGMSLGAKGAAGPLPSAVQNLQHAFL	1080						
Qy	1081	KLTRHRVTVPLIGSLRTRATQTLSRKLPGTTLTALEAANPAPSDPKTILD1132	1132						
Db	1081	KLTRHRVTVPLIGSLRTRATQTLSRKLPGTTLTALEAANPAPSDPKTILD1132	1132						
Qy	541	LAKFLHWLMSVYVYELLRSFYYTETTEFKNLFFYRKSYWKLQSIGITROHLKRVQRE	600						
Db	541	LAKFLHWLMSVYVYELLRSFYYTETTEFKNLFFYRKSYWKLQSIGITROHLKRVQRE	600						
Qy	601	LSAEVROREARPAALLTSRLETRIPKPDGLRPIVNMMDYVUGARTFREKRAERTSRVKA	660						
Db	601	LSAEVROREARPAALLTSRLETRIPKPDGLRPIVNMMDYVUGARTFREKRAERTSRVKA	660						
Qy	661	LSFVNLAYERARRGLGASVGLGDDIHAWRTVLRVRAQDPPELYFVYDVTGAYDT1	720						
Db	661	LSFVNLAYERARRGLGASVGLGDDIHAWRTVLRVRAQDPPELYFVYDVTGAYDT1	720						

RESULT 2  
JS-09-749-7281  
Sequence 31  
Patent No. U.S. 5,000,000  
GENERAL INFORMATION  
APPLICANT: APPLICANT:

Db 661 LFSVLYNERARRPGIIGASVGLDDIIRAWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720  
 Qy 721 PQDRLTEVIASIIKPKONTYCVRAYAVVQRAAHGHYRKAFKSHVSTLTDLOPVMQFVAHL 780  
 Db 721 PQDRLTEVIASIIKPKONTYCVRAYAVVQRAAHGHYRKAFKSHVSTLTDLOPVMQFVAHL 780  
 Qy 781 QETSPRLDAVVIQESSLNEASSGLFDVFLRFMCHHAVRIGKSYVQCGIPQGSLTSLT 840  
 Db 781 QETSPRLDAVVIQESSLNEASSGLFDVFLRFMCHHAVRIGKSYVQCGIPQGSLTSLT 840  
 Qy 841 LCSLCYGDMEKLFAGIRRDGCLLRLVDDFLVTPPHLTHAKTFPLRLTURGVPEYGCVNLL 900  
 Db 841 LCSLCYGDMEKLFAGIRRDGCLLRLVDDFLVTPPHLTHAKTFPLRLTURGVPEYGCVNLL 900  
 Qy 901 RKTIVNPFVVEDBALGTAFVOMPAHGFPMCGLLDRTTLEQSDYSYARTSIRASLT 960  
 Db 901 RKTIVNPFVVEDBALGTAFVOMPAHGFPMCGLLDRTTLEQSDYSYARTSIRASLT 960  
 Qy 961 NRGFKAQRNMRKLFPGVRLKCHSLFLDLOVNSLOTCVNTIYKILLQAYRFHACVQLP 1020  
 Db 961 NRGFKAQRNMRKLFPGVRLKCHSLFLDLOVNSLOTCVNTIYKILLQAYRFHACVQLP 1020  
 Qy 1021 PHQQWKNPTEFLRVTISDTASLCLYSTIKAKNAGMSLGAKGAGPLPSEAVQLCHQAFLL 1080  
 Db 1021 PHQQWKNPTEFLRVTISDTASLCLYSTIKAKNAGMSLGAKGAGPLPSEAVQLCHQAFLL 1080  
 Qy 1081 KLTTRHVTYVPLLSLRTAQTLSRKLPGTTLTALEAAANPALPSDFKTLID 1132  
 Db 1081 KLTTRHVTYVPLLSLRTAQTLSRKLPGTTLTALEAAANPALPSDFKTLID 1132

RESULT 3  
 Sequence US-09-843-676-225  
 Application US/098433676  
 Patent No. US2002164786A1  
 GENERAL INFORMATION:  
 APPLICANT: Cech, Thomas R.  
 Lingner, Joachim  
 Nakamura, Toru  
 Chapman, Karen B.  
 Morin, Gregg B.  
 Harley, Calvin  
 Andrews, William H.  
 TITLE OF INVENTION: No. US20020164786A1 Telomerase  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, 8th Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States of America  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/854,050  
 FILING DATE: 26-APR-2001  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/854,050  
 FILING DATE: 09-MAY-1997  
 APPLICATION NUMBER: US/08/846,017  
 FILING DATE: 25-APR-1997  
 APPLICATION NUMBER: US/08/844,419  
 FILING DATE: 18-APR-1997  
 APPLICATION NUMBER: US/08/724,643  
 FILING DATE: 01-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Apple, Randolph T.  
 REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 225:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 225:  
 US-09-843-676-225:  
 Query Match 100.0%; Score 5961; DB 9; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Query 1 MPRAPCRAVRLSLRSHYREVLPATFVRLGPQGMWLVORGDPAAFLALVQAQCLVCVPW 60  
 Db 1 MPRAPCRAVRLSLRSHYREVLPATFVRLGPQGMWLVORGDPAAFLALVQAQCLVCVPW 60  
 Qy 61 DARPPEAAPFPRQVCLKEVAVLQRLCERGAQVNLAFQALDUCRGCPPEAFTSVR 120  
 Db 61 DARPPEAAPFPRQVCLKEVAVLQRLCERGAQVNLAFQALDUCRGCPPEAFTSVR 120  
 Qy 121 SYLPNTVTDALRGSAWGLLRLVACALFVLPAPSCAYQVCGPPLYQLGA 180  
 Db 121 SYLPNTVTDALRGSAWGLLRLVACALFVLPAPSCAYQVCGPPLYQLGA 180  
 Qy 181 ATQARPPHASGPRLGCERAWHNSVREAGVPLPGLPAPGARRGGSASRSLPPLPKPRRR 240  
 Db 181 ATQARPPHASGPRLGCERAWHNSVREAGVPLPGLPAPGARRGGSASRSLPPLPKPRRR 240  
 Qy 241 GAAPPEPERTVQGGSWAHPERTGSDRGICVVSPPARPAEATSLGALSGTSHSPSGV 300  
 Db 241 GAAPPEPERTVQGGSWAHPERTGSDRGICVVSPPARPAEATSLGALSGTSHSPSGV 300  
 Qy 301 RQHAGGPPSTSRRPSPRPWDTCPPYTAETKHFLLYSSSGDKEQLRPSFLSSLRPSTGARRL 360  
 Db 301 RQHAGGPPSTSRRPSPRPWDTCPPYTAETKHFLLYSSSGDKEQLRPSFLSSLRPSTGARRL 360  
 Qy 361 VETIFLGSRPPMMPGPRLPQPYWQMPFLLELGNHAQCPYGVLLKTHCPRAAVT 420  
 Db 361 VETIFLGSRPPMMPGPRLPQPYWQMPFLLELGNHAQCPYGVLLKTHCPRAAVT 420  
 Qy 421 PAAGTCAREPKQGSTAAPPEBDTDRRLVQLLRQHNSPPQYGYTRACIQLVPLGWS 480  
 Db 421 PAAGTCAREPKQGSTAAPPEBDTDRRLVQLLRQHNSPPQWVGFTRACIQLVPLGWS 480  
 Qy 481 RHNERFLRNTKKFISLGKHAKLSLQELITKMSVRDCANLRRSPGVGCVPAAEHLREEI 540  
 Db 481 RHNERFLRNTKKFISLGKHAKLSLQELITKMSVRDCANLRRSPGVGCVPAAEHLREEI 540  
 Qy 541 LAKFELHWMSSVYVWELLRSPPVETTFQKNRLLFYRKSVWSKLSIGIRQLRKVQRL 600  
 Db 541 LAKFELHWMSSVYVWELLRSPPVETTFQKNRLLFYRKSVWSKLSIGIRQLRKVQRL 600  
 Qy 601 LSEAEVTRQHREARPALTSURFVKPDKGIRPPIVMDYVQGARTPRREKAERLTSRVKA 660  
 Db 601 LSEAEVTRQHREARPALTSURFVKPDKGIRPPIVMDYVQGARTPRREKAERLTSRVKA 660  
 Qy 661 LFSVLYNERARRPGIIGASVGLDDIIRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720  
 Db 661 LFSVLYNERARRPGIIGASVGLDDIIRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720  
 Qy 721 PQDRLTEVIASTIKPQNTYCVRRAVVKAHGHYRKAFKSHVSTATDLOPYMROFVAHL 780  
 Db 721 PQDRLTEVIASTIKPQNTYCVRRAVVKAHGHYRKAFKSHVSTATDLOPYMROFVAHL 780  
 Qy 781 QETSPRLDAVVIQESSLNEASSGLFDVFLRFMCHHAVRIGKSYVQCGIPQGSILSTL 840  
 Db 781 QETSPRLDAVVIQESSLNEASSGLFDVFLRFMCHHAVRIGKSYVQCGIPQGSILSTL 840

RESULT 4

US-09-953-052-2

Sequence - 2, Application US/0953052

Patent No. 720020173476A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Antisense Compositions for Detecting and Inhibiting Telomerase Reverse Transcriptase

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

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ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/953,052

FILING DATE: 14-Sep-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052,919

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/914,549

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/974,584

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Parent, Annette S.

REGISTRATION NUMBER: 42,058

REFERENCE/DOCKET NUMBER: 015389-003600US

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INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1132 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-953-052-2

Query Match 100.0%; Score 5961; DB 9; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPPRPRCAVRSLRSHYREVPLATEVRLGPQWRLVQRQDPAARALVAQCLVCPW 60

Db 1 MPPRPRCAVRSLRSHYREVPLATEVRLGPQWRLVQRQDPAARALVAQCLVCPW 60

Qy 61 DARPPAAPSFRQVSCILKELVARVLQICERGAKVNLAFGFLALDGARGGPBEAFTTSVR 120

Db 61 DARPPAAPSFRQVSCILKELVARVLQICERGAKVNLAFGFLALDGARGGPBEAFTTSVR 120

Qy 121 SYLPLNTVDAIGSGANGLLPPLRGGDDVYLHARCAFLVAPSCAYQVCCPPLYQLG 180

Db 121 SYLPLNTVDAIGSGAWGLLJRRGVDDVYLHARCAFLVAPSCAYQVCCPPLYQLG 180

Qy 181 ATQRPPPHASGPRRGGCERAWNHSYREAGYPLGLPAGARRGGASRS1PLPKPRR 240

Db 181 ATQRPPPHASGPRRGGCERAWNHSYREAGYPLGLPAGARRGGASRS1PLPKPRR 240

Qy 241 GAPEPEPTVPGQGSWAHPGRTRGPSDRGFCVVSPARPAEATSLEGALSGTRHSHPSVG 300

Db 241 GAPEPEPTVPGQGSWAHPGRTRGPSDRGFCVVSPARPAEATSLEGALSGTRHSHPSVG 300

Qy 301 ROHAGPPSTSRPRPMDTTPCPVYAEHKELYSGDKEOLRPSLTSRPLTGARRL 360

Db 301 ROHAGPPSTSRPRPMDTTPCPVYAEHKELYSGDKEQRLPSLTSRPLTGARRL 360

Qy 361 VETIFLGSRPNMPTPRLPPLPQRYWQMRPLFLLEJGNHAQCPGVYLKTHCPPLRAVT 420

Db 361 VETIFLGSRPNMPTPRLPPLPQRYWQMRPLFLLEJGNHAQCPGVYLKTHCPPLRAVT 420

Qy 421 PAAGVCAREKQGSVAPEEEDTPRLVQLRHQHSPWQVYGFVACRLRVPGLWGS 480

Db 421 PAAGVCAREKQGSVAPEEEDTPRLVQLRHQHSPWQVYGFVACRLRVPGLWGS 480

Qy 481 RHNERFLRNTYKFKISLGKHAKLSSLBLTWNMSVRCAWLRSRGYCPAAEHRLREEI 540

Db 481 RHNERFLRNTYKFKISLGKHAKLSSLBLTWNMSVRCAWLRSRGYCPAAEHRLREEI 540

Qy 541 LAKFLFLWLMSTYYVVELRSSEFTTFOKRLFLFVRSYNSKLSQSIGIROLHKVQYLE 600

Db 541 LAKFLFLWLMSTYYVVELRSSEFTTFOKRLFLFVRSYNSKLSQSIGIROLHKVQYLE 600

Qy 601 LSEAVYRQHREARPALTSRFLPKPDGLRPIVMDVYVGARTPREKAERLTSRVKA 660

Db 601 LSEAVYRQHREARPALTSRFLPKPDGLRPIVMDVYVGARTPREKAERLTSRVKA 660

Qy 661 LFSVNLAYERAERPGLGASVILGLD1IHRMRTFVLRVAQDPPPFLFVVDVTGAYDTI 720

Db 661 LFSVNLAYERAERPGLGASVILGLD1IHRMRTFVLRVAQDPPPFLFVVDVTGAYDTI 720

Qy 721 PQDRLTEVIASIIKPONTYCVRYYAVQXAVQXAHGHTRAFKSHVSTLTDQPYMRQQFVAHL 780

Db	721	PQDRLETEVIASTIKPQNTYCVRRYAVVQRAAHHYRKAFKSFHVSITDLDQPMYQFVALI	780	RE	301	ROHHAGPPSTSRPFPWDTCPPVYAEIHKFLYSSGDKEQLRSPFLSSLRPLSLTGARRL
Qy	781	QBTSPRDVAVIEQSSSLNEASSGLPFDVFLRPMCHAVLRGKSTVQCGIPQGSILSTL	840	QY	361	VETIFLGSRWPMPGTPLLRLPQYQWQRPFLFLLGNEAQCPYGVLLKTHCPRAAVT
Db	781	QBTSPRDVAVIEQSSSLNEASSGLPFDVFLRPMCHAVLRGKSTVQCGIPQGSILSTL	840	RE	361	VETIFLGSRWPMPGTPLLRLPQYQWQRPFLFLLGNEAQCPYGVLLKTHCPRAAVT
Qy	841	LCSLCYGMENKLFAIGTRDGLLRLYDFFLVTPLTHARTFLRTLTVRGYPEYGCVNLL	900	QY	421	PAAGTCAREKPOGSVAAPEEEDTDPRLYQLLRHOSSPMQVYGFTRACIIRLVPGLWGS
Db	841	LCSLCYGMENKLFAIGTRDGLLRLYDFFLVTPLTHARTFLRTLTVRGYPEYGCVNLL	900	RE	421	PAAGTCAREKPOGSVAAPEEEDTDPRLYQLLRHOSSPMQVYGFTRACIIRLVPGLWGS
Qy	901	RKTVNNEPVDEALGGTAFYQMPAHLFPMCGLJLDTPLTEQSYSSARTSPASLTF	960	QY	481	RHNBFRFLNTKKTISLGKHAUKLSQELTWMKMSYRDCANLRSRPGVGYCPAAEHLREEL
Db	901	RKTVNNEPVDEALGGTAFYQMPAHLFPMCGLJLDTPLTEQSYSSARTSPASLTF	960	RE	481	RHNBFRFLNTKKTISLGKHAUKLSQELTWMKMSYRDCANLRSRPGVGYCPAAEHLREEL
Db	961	NRGFXAGRNMKRKLFCVLRKCHSLFLDLOVNSLOTVCNTYKULLQAYRFHACVLQD	1020	QY	541	LAKFTHWLMSSVYVYELLRSPPYVETTEFQKNRLFPRYKSVWSKLQCGISIGRQHLLKRVQVLR
Db	961	NRGFXAGRNMKRKLFCVLRKCHSLFLDLOVNSLOTVCNTYKULLQAYRFHACVLQD	1020	RE	541	LAKFTHWLMSSVYVYELLRSPPYVETTEFQKNRLFPRYKSVWSKLQCGISIGRQHLLKRVQVLR
Qy	1021	FHQQWKNPTEFLRVTSATSLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHOAFLJ	1080	QY	601	LSEAVRQHREARPALTSBLRFKPGDGLRPIYMDYVQGARTFREKRAERLTSRVKA
Db	1021	FHQQWKNPTEFLRVTSATSLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHOAFLJ	1080	RE	601	LSEAVRQHREARPALTSBLRFKPGDGLRPIYMDYVQGARTFREKRAERLTSRVKA
Qy	1081	KLTTRHRTVYIPLGSRTAQTQLSRKLPGTITLAEANANPALSDFKTLID	1132	QY	661	LFSVNVYERARRPGILGASVYGLDODIHRRAWRTFVLRVRAQDPPPEFLYKVDVYGA
Db	1081	KLTTRHRTVYIPLGSRTAQTQLSRKLPGTITLAEANANPALSDFKTLID	1132	RE	661	LFSVNVYERARRPGILGASVYGLDODIHRRAWRTFVLRVRAQDPPPEFLYKVDVYGA
Qy	721	PQDRLETEVIASTIKPQNTYCVRRYAVVQKAAHGHYRKAKPSHVSTLTDLQPMQFV AHL	780	QY	721	PQDRLETEVIASTIKPQNTYCVRRYAVVQKAAHGHYRKAKPSHVSTLTDLQPMQFV AHL
Db	721	PQDRLETEVIASTIKPQNTYCVRRYAVVQKAAHGHYRKAKPSHVSTLTDLQPMQFV AHL	780	RE	721	PQDRLETEVIASTIKPQNTYCVRRYAVVQKAAHGHYRKAKPSHVSTLTDLQPMQFV AHL
Qy	781	QETSSLRDAVIEQSSSLNEASSGFDVFLRFMCHAVLRGKSVQCGIPQGSILSTL	840	QY	781	QETSSLRDAVIEQSSSLNEASSGFDVFLRFMCHAVLRGKSVQCGIPQGSILSTL
Db	781	QETSSLRDAVIEQSSSLNEASSGFDVFLRFMCHAVLRGKSVQCGIPQGSILSTL	840	RE	781	QETSSLRDAVIEQSSSLNEASSGFDVFLRFMCHAVLRGKSVQCGIPQGSILSTL
Qy	841	LCSTLCYGMENKLFAIGTRDGLLRLVDDFLVYTFHLTHAKTFLRTLVRGVPYECVVNL	900	QY	841	LCSTLCYGMENKLFAIGTRDGLLRLVDDFLVYTFHLTHAKTFLRTLVRGVPYECVVNL
Db	841	LCSTLCYGMENKLFAIGTRDGLLRLVDDFLVYTFHLTHAKTFLRTLVRGVPYECVVNL	900	RE	841	LCSTLCYGMENKLFAIGTRDGLLRLVDDFLVYTFHLTHAKTFLRTLVRGVPYECVVNL
Qy	901	RKTVNFPVDEALGTAFYQMPAHGLFPMCGLLDTRLEVQSDYSSARTSIRASLTF	960	QY	901	RKTVNFPVDEALGTAFYQMPAHGLFPMCGLLDTRLEVQSDYSSARTSIRASLTF
Db	901	RKTVNFPVDEALGTAFYQMPAHGLFPMCGLLDTRLEVQSDYSSARTSIRASLTF	960	RE	901	RKTVNFPVDEALGTAFYQMPAHGLFPMCGLLDTRLEVQSDYSSARTSIRASLTF
Qy	961	NRGFXAGRNMKRKLFCVLRKCHSLFLDQVNLQYRFHACVLQD	1020	QY	961	NRGFXAGRNMKRKLFCVLRKCHSLFLDQVNLQYRFHACVLQD
Db	961	NRGFXAGRNMKRKLFCVLRKCHSLFLDQVNLQYRFHACVLQD	1020	RE	961	NRGFXAGRNMKRKLFCVLRKCHSLFLDQVNLQYRFHACVLQD
Qy	1021	FHQQWKNPTEFLVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHOAFL	1080	QY	1021	FHQQWKNPTEFLVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHOAFL
Db	1021	FHQQWKNPTEFLVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHOAFL	1080	RE	1021	FHQQWKNPTEFLVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHOAFL
Qy	1081	KLTTRHRTVYPLGSRTAQTQLSRKLPGTITLAEANANPALSDFKTLID	1132	QY	1081	KLTTRHRTVYPLGSRTAQTQLSRKLPGTITLAEANANPALSDFKTLID
Db	1081	KLTTRHRTVYPLGSRTAQTQLSRKLPGTITLAEANANPALSDFKTLID	1132	RE	1081	KLTTRHRTVYPLGSRTAQTQLSRKLPGTITLAEANANPALSDFKTLID
Qy	61	DARPPPAAPSFQVSCILKELVARYLQRLCERGAKNVLAFGLDARGCPPEAFTTSYR	120	QY	61	RESULT 6
Db	61	DARPPPAAPSFQVSCILKELVARYLQRLCERGAKNVLAFGLDARGCPPEAFTTSYR	120	RE	61	US-10-053-758-225
Qy	121	SYLPNTVTDALRGSGAWGLLRRVSDDVYLHARCAFLVYDPLKQYCGPFLYQGA	180	QY	121	SEQUENCE 225; Application US/10053758
Db	121	SYLPNTVTDALRGSGAWGLLRRVSDDVYLHARCAFLVYDPLKQYCGPFLYQGA	180	RE	121	SEQUENCE 225; Application US/10053758
Qy	181	ATQARPPHASGPRRLGCBARNHSVRQGVPGLPAPARRGGSASSRLPLPKRPR	240	QY	181	GENERAL INFORMATION:
Db	181	ATQARPPHASGPRRLGCBARNHSVRQGVPGLPAPARRGGSASSRLPLPKRPR	240	RE	181	Publication No. US20030032075A1
Qy	241	GAAPEPERTPVQGGSWAHPGRTRGSDRGFCVSPARPAEATSLEGALSGTRISHPSYVG	300	QY	241	APPLICANT: Cech, Thomas R.
Db	241	GAAPEPERTPVQGGSWAHPGRTRGSDRGFCVSPARPAEATSLEGALSGTRISHPSYVG	300	RE	241	Lingner, Joachim
Qy	301	ROHHAGPPSTSRPFPWDTCPPVYAEIHKFLYSSGDKEQLRSPFLSSLRPLSLT GARRL	360	QY	301	Nakamura, Toru

STATE: California  
CITY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/053, 758  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854, 050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851, 843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846, 017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844, 419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724, 643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 105389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 225:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1132 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 225:  
US-10-053-758-225

Query Match 100.0% Score 5961; DB 14; Length 1132;  
Best Local Similarity 100.0% Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPCRAVSLLSRHYREVPLATEFVRQLGPQWWRLYQRGDDAAFLVALAACQIJCVCFW 60  
Db 1 MPRAPCRAVSLLSRHYREVPLATEFVRQLGPQWWRLYQRGDDAAFLVALAACQIJCVCFW 60

Qy 61 DARPPAAPSQVSLLKELVALRQLCERAKNVLAFALLDARGGPPEAFTTSYR 120  
Db 61 DARPPAAPSQVSLLKELVALRQLCERAKNVLAFALLDARGGPPEAFTTSYR 120

Qy 121 SYLPNTVTDAIRGSAGWGLLRRVGDVLHLLARCALFVLYVAPSCAYCVCGLPGLGA 180  
Db 121 SYLPNTVTDAIRGSAGWGLLRRVGDVLHLLARCALFVLYVAPSCAYCVCGLPGLGA 180

Qy 181 ATQARPPPHASGPRRGLCERAMHNSVREANGVPLGLPAGGRRGGSASRSLPLPKRPR 240  
Db 181 ATQARPPPHASGPRRGLCERAMHNSVREANGVPLGLPAGGRRGGSASRSLPLPKRPR 240

Qy 241 GAAPPEERTPVQGGSWAHPGTRGSDRGCVSVSPARPEEATSGALGTRHSPVSG 300  
Db 241 GAAPPEERTPVQGGSWAHPGTRGSDRGCVSVSPARPEEATSGALGTRHSPVSG 300

Qy 301 RQHAGGPPSTSRRPWRDTPCPVYATKHFLYSSGDKEQLRPSFLSSLRPLSTGARL 360  
Db 301 RQHAGGPPSTSRRPWRDTPCPVYATKHFLYSSGDKEQLRPSFLSSLRPLSTGARL 360

Qy 361 VETIFGSRPMPGTPPRRPLRPPQWMPFLLELGNAQCPYGVLLKTHCPLRAVT 420  
Db 361 VETIFGSRPMPGTPPRRPLRPPQWMPFLLELGNAQCPYGVLLKTHCPLRAVT 420

Qy 421 PAAGVGCAREKPOGSVAAPPEEFTDPRRLVQLRQHSSPQVYGVRACLRLVPPGLNGS 480

Db 421 PAAGVGCAREKPOGSVAAPPEEFTDPRRLVQLRQHSSPQVYGVRACLRLVPPGLNGS 480

Qy 481 RHNERRFLENTKKEPISLGKHAKSLSQELTWMSSYRDCAWLRSRPGVGCPAABHRLREI 5  
Db 481 RHNERRFLENTKKEPISLGKHAKSLSQELTWMSSYRDCAWLRSRPGVGCPAABHRLREI 5

Qy 541 LAKELHWMMSVYVLLRSFFYTTETTFOQRNLFYRKSWSLQSISIGTROHLKRVQLE 6  
Db 541 LAKELHWMMSVYVLLRSFFYTTETTFOQRNLFYRKSWSLQSISIGTROHLKRVQLE 6

Qy 601 LSEAEVROHREARPALTSRSLRFTPKPDGLRPTVNMDDYVGAETFRERKABLTSRVKA 66  
Db 601 LSEAEVROHREARPALTSRSLRFTPKPDGLRPTVNMDDYVGAETFRERKABLTSRVKA 66

Qy 661 LFSVLYNERARRPGLGASVGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDTGAYDTI 72  
Db 661 LFSVLYNERARRPGLGASVGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDTGAYDTI 72

Qy 721 PQDLTEVIAISIKPQNTYCVRHYAVVOKAAGHVRKAFKSHYSTLTDQPMRQFV AHL 78  
Db 721 PQDLTEVIAISIKPQNTYCVRHYAVVOKAAGHVRKAFKSHYSTLTDQPMRQFV AHL 78

Qy 781 QETSPLRDAVIEQSSSLNEASGGLFDPYFLRMCHHAIRGKSYVOCQGIPGOSLSTL 80  
Db 781 QETSPLRDAVIEQSSSLNEASGGLFDPYFLRMCHHAIRGKSYVOCQGIPGOSLSTL 80

Qy 841 LCSLCYGDGMENKLFGAIRDGLLRLYVDDFLVTPHLTHAKTFLRFLTRVGRGPBYCGVNL 90  
Db 841 LCSLCYGDGMENKLFGAIRDGLLRLYVDDFLVTPHLTHAKTFLRFLTRVGRGPBYCGVNL 90

Qy 901 RKTUVNFPVDEALGGTAFVQMPAHGLPWCGILLDRTLEQDSSYARTSIRASITF 96  
Db 901 RKTUVNFPVDEALGGTAFVQMPAHGLPWCGILLDRTLEQDSSYARTSIRASITF 96

Qy 961 NRGFKAAGRNMRRKLFGVRLRKCHSLFLDQNSLQVTCNTIYKILLQAYRFHACVLOP 100  
Db 961 NRGFKAAGRNMRRKLFGVRLRKCHSLFLDQNSLQVTCNTIYKILLQAYRFHACVLOP 100

Qy 1021 FHQQWKNPTEFLRVSIDASLICSYLISILKAKNAGMSLGAKGAQGLPSEAVONWICHOAFL 10  
Db 1021 FHQQWKNPTEFLRVSIDASLICSYLISILKAKNAGMSLGAKGAQGLPSEAVONWICHOAFL 10

Qy 1081 KLTTRHRTTYVPLJGSLRATAQTQSLRKLPGTLTVALEAAANPALSQDKTILD 1132  
Db 1081 KLTTRHRTTYVPLJGSLRATAQTQSLRKLPGTLTVALEAAANPALSQDKTILD 1132

RESULT 7  
US-10-208-243-2  
; Sequence 2, Application US/10208243  
; Publication No. US20030044394A1  
; GENERAL INFORMATION:  
; APPLICANT: Gatera, Federico C.A.  
; APPLICANT: Geron Corporation  
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune  
; TITLE OF INVENTION: Response to a Telomerase Antigen  
; FILE REFERENCE: 015389-03500PC  
; CURRENT APPLICATION NUMBER: US/10/208-243  
; CURRENT FILING DATE: 2002-07-30  
; PRIOR APPLICATION NUMBER: US/09/675, 321  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/112, 006  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 1  
; LENGTH: 1132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-208-243-2

Query Match	100.0%	Score 5961;	DB 14;	Length 1132;	
Best Local Similarity	100.0%	Pred. No. 0;			
Matches 1132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
/	1	MPRAPCRARVSLRSHYREVPLATEVRLGPQWRVLRGDPAAFRALVAQCLVCPW	60		
/	1	MPRAPCRARVSLRSHYREVPLATEVRLGPQWRVLRGDPAAFRALVAQCLVCPW	60		
Y	61	DARPPAAFSFROVSCLKELEVARYLQLCERGAKNVLANGFALLDGARGPPEAFTTSVR	120	RESULT 8	Db
o	61	DARPPAAFSFROVSCLKELEVARYLQLCERGAKNVLAFCAFDLGDARGPPEAFTTSVR	120	US-10-054-295-225	Qy
Y	121	SYLPNTVTDLRGSSAWGLLRLRGGDDVNLHLLARCALPVLVAPSCAYQVGPPLYQLGA	180	; Sequence 225, Application US/10054295	Db
o	121	SYLPNTVTDLRGSSAWGLLRLRGGDDVNLHLLARCALPVLVAPSCAYQVGPPLYQLGA	180	; Publication No. US20030044953A1	
Y	181	ATOARPPPHASGPRRRLGCRERAWHNSVREAGVYPLGPAPGARRGGSASRSLPLPKRPR	240	; GENERAL INFORMATION:	
o	181	ATOARPPPHASGPRRRLGCRERAWHNSVREAGVYPLGPAPGARRGGSASRSLPLPKRPR	240	; APPLICANT: Cech, Thomas R.	
Y	241	GAAPERTVPGQGSWAHPRTGRPSDRGTCVVSPARAEATSLLEGALSTGRSHSPVG	300	; ADDRESS: Nakamura, Toru	
o	241	GAAPERTVPGQGSWAHPRTGRPSDRGTCVVSPARAEATSLLEGALSTGRSHSPVG	300	; Chapman, Karen B.	
Y	301	ROHAGPPSTSRPRPWDTFCPPYTAETKFLYSSGDKBQLRSPFLSSRPSLTGARRL	360	; Morin, Gregg B.	
o	301	ROHAGPPSTSRPRPWDTFCPPYTAETKFLYSSGDKBQLRSPFLSSRPSLTGARRL	360	; Harley, Calvin	
Y	361	VETIFLGSSWMPMPCTPRLPLRPLPORYWQWMPBLPLFLLGHQAQCPYGVLLKTHCP1RAAVT	420	; Andrews, William H.	
o	361	VETIFLGSSWMPMPCTPRLPLRPLPORYWQWMPBLPLFLLGHQAQCPYGVLLKTHCP1RAAVT	420	; TITLE OF INVENTION: US 20010044953A1 el. Telomerase	
Y	421	PAAGYCAREKPOGSVAAPBEEFTDPRRLVQLRQHSSPQVYGFVACRLRVPGLWCS	480	; NUMBER OF SEQUENCES: 225	
o	421	PAAGYCAREKPOGSVAAPBEEFTDPRRLVQLRQHSSPQVYGFVACRLRVPGLWCS	480	; CORRESPONDENCE ADDRESS:	
Y	481	RHNERFLRNTKKFISLGRHAKLSQLETLWMSYRDCAMVLRSPGCVPAEHLRLEET	540	; ADDRESSEE: Townsend and Townsend and Crew LLP	
o	481	RHNERFLRNTKKFISLGRHAKLSQLETLWMSYRDCAMVLRSPGCVPAEHLRLEET	540	; STREET: Two Embarcadero Center, 8th Floor	
Y	541	LAKELHWLMSVYVYELLRSFYYTETTEFQNLFFYRKSVWSKLQSIGTRQH1KRVOLRE	600	; CITY: San Francisco	
o	541	LAKELHWLMSVYVYELLRSFYYTETTEFQNLFFYRKSVWSKLQSIGTRQH1KRVOLRE	600	; STATE: California	
Y	601	LSEAEVROQHEARPALITSLRFLPKPDGIRP1VNMDDYVGAFTFREKERAELTSRVKA	660	; COUNTRY: United States of America	
o	601	LSEAEVROQHEARPALITSLRFLPKPDGIRP1VNMDDYVGAFTFREKERAELTSRVKA	660	; ZIP: 94111	
Y	721	PODRLTEVAAISIKPONTIVCRRAYVQKAAHGYRKAKPSHVSHTLTDQPYNRQFV AHL	720	; COMPUTER READABLE FORM:	
o	721	PODRLTEVAAISIKPONTIVCRRAYVQKAAHGYRKAKPSHVSHTLTDQPYNRQFV AHL	720	; MEDIUM TYPE: Floppy disk	
Y	721	PODRLTEVAAISIKPONTIVCRRAYVQKAAHGYRKAKPSHVSHTLTDQPYNRQFV AHL	720	; COMPUTER: IBM PC compatible	
o	721	PODRLTEVAAISIKPONTIVCRRAYVQKAAHGYRKAKPSHVSHTLTDQPYNRQFV AHL	720	; OPERATING SYSTEM: PC-DOS/M-DOS	
Y	781	QETSPSLRDAVVIQESSLNFASGLFDVFRMCHAVRLRGKSYVQOCQIPQSSILSTL	840	; SOFTWARE: Patent In Release #1.0, Version #1.30	
o	781	QETSPSLRDAVVIQESSLNFASGLFDVFRMCHAVRLRGKSYVQOCQIPQSSILSTL	840	; CURRENT APPLICATION DATA:	
Y	841	LCSLCYGDMMNLKFLGIRIGRQLLRLVDDFLVTPHLTHAKTFLRTLVCPYEGCVWNL	900	; APPLICATION NUMBER: US/10/054 , 295	
o	841	LCSLCYGDMMNLKFLGIRIGRQLLRLVDDFLVTPHLTHAKTFLRTLVCPYEGCVWNL	900	; FILING DATE: 18-Jan-2002	
Y	901	RKTIVNPFVEDAEGGTAFTQMPAHGLFPQCGLLDTRLEQDSSYSSARTS1RASLT	960	; CLASSIFICATION: 53-6	
o	901	RKTIVNPFVEDAEGGTAFTQMPAHGLFPQCGLLDTRLEQDSSYSSARTS1RASLT	960	; PRIORITY APPLICATION DATA:	
Y	961	NRGFKAGRANNRKLFGVLRKCHSLFLDQVNSLQTVCTN1YK1L0QYRFHACVQLP	1020	; APPLICATION NUMBER: 08/854 , 050	
o	961	NRGFKAGRANNRKLFGVLRKCHSLFLDQVNSLQTVCTN1YK1L0QYRFHACVQLP	1020	; FILING DATE: <Unknown>	
Y	1080	100.0% ; Score 5961;	DB 14;	Length 1132;	Qy
Y	1080	Best Local Similarity 100.0%; Pred. No. 0;	Mismatches 0;	Indels 0;	Gaps 0;
Y	1	MPRAPCRARVSLRSHYREVPLATEVRLGPQWRVLRGDPAAFRALVAQCLVCPW	60	1 MPRAPCRARVSLRSHYREVPLATEVRLGPQWRVLRGDPAAFRALVAQCLVCPW	Db
Y	1	MPRAPCRARVSLRSHYREVPLATEVRLGPQWRVLRGDPAAFRALVAQCLVCPW	60	1 MPRAPCRARVSLRSHYREVPLATEVRLGPQWRVLRGDPAAFRALVAQCLVCPW	Qy
Y	61	DARPPAAFSFROVSCLKELEVARYLQLCERGAKNVLANGFALLDGARGPPEAFTTSVR	120	61 DARPPAAFSFROVSCLKELEVARYLQLCERGAKNVLANGFALLDGARGPPEAFTTSVR	

61 DARPPAAPSFRQVSCLKEVLRVQLCERGAKNVLAFCGFALLDARGGPEAFTTSV 120  
 121 SYLPNTVTDAIRGSGAWGLLJRRVGDVYHLLARCAFLVAPSCAYQVCGPPLYQVGA 180  
 121 SYLPNTVTDAIRGSGAWGLLJRRVGDVYHLLARCAFLVAPSCAYQVCGPPLYQVGA 180  
 181 ATQARPPPHASGPERRRLGCRGAAWHSYREAGVPLGLPAGARRGGSAARSLSLPKRRR 240  
 181 ATQARPPPHASGPERRRLGCRGAAWHSYREAGVPLGLPAGARRGGSAARSLSLPKRRR 240  
 241 GAAPEPRTPVQGSMAPGPRTRGSDRGICVSPARPEEATSLLEGALSGTRHSHPSVG 300  
 241 GAAPEPRTPVQGSMAPGPRTRGSDRGICVSPARPEEATSLLEGALSGTRHSHPSVG 300  
 301 ROHHAGPSPSRPPEWDTPCPVPPVAAETKHFYLSGDKKEQRLRSPFLSSLRPSTLGARBL 360  
 301 RQHHAGPSPSRPPEWDTPCPVPPVAAETKHFYLSGDKKEQRLRSPFLSSLRPSTLGARBL 360  
 361 VETIFGSRPMPMGPGRPLRPLPQRYWQMPRLPELFLGNGHAQCPYGVNLKTHCPLRAVT 420  
 361 VETIFGSRPMPMGPGRPLRPLPQRYWQMPRLPELFLGNGHAQCPYGVNLKTHCPLRAVT 420  
 421 PAAGVCAKEPKQGSYAAPEEEDTDPRLVOLLRQHSSPQVYGVPRACRLRVPGLMGS 480  
 421 PAAGVCAKEPKQGSYAAPEEEDTDPRLVOLLRQHSSPQVYGVPRACRLRVPGLMGS 480  
 481 RHNERRFLRNTKFKFISLGKAHLKSLQELTWKMSVYDCAWLRRSPVGCVCPAAEHLRBEI 540  
 481 RHNERRFLRNTKFKFISLGKAHLKSLQELTWKMSVYDCAWLRRSPVGCVCPAAEHLRBEI 540  
 541 LAKEFLHWLMSVYVYLLRSFYYVETTFQKNRLPFYRKSYWSKLQSIGTRQHLKRVQRE 600  
 541 LAKEFLHWLMSVYVYLLRSFYYVETTFQKNRLPFYRKSYWSKLQSIGTRQHLKRVQRE 600  
 601 LSEAEVQRHNEARPALLTSURF1PKDGLRPIVNMDDYVGarFRRERAAELTSRKKA 660  
 601 LSEAEVQRHNEARPALLTSURF1PKDGLRPIVNMDDYVGarFRRERAAELTSRKKA 660  
 661 LFSVINYERARRPGLGASVGLDDIHRAWRTFVLRQAQDPPPELYFKVDTGAYDTI 720  
 661 LFSVINYERARRPGLGASVGLDDIHRAWRTFVLRQAQDPPPELYFKVDTGAYDTI 720  
 721 PQDRLETVIASI1KQPNTYCVRVYAVVQKAHHGIVRKAKSHVSTLTDIQPYMRQFV AHL 780  
 721 PQDRLETVIASI1KQPNTYCVRVYAVVQKAHHGIVRKAKSHVSTLTDIQPYMRQFV AHL 780  
 781 QETSPLRDAVIEQSSSLNEASSGFLDVRMCHAVRIGKSYVQCGGIPOSSILSTL 840  
 781 QETSPLRDAVIEQSSSLNEASSGFLDVRMCHAVRIGKSYVQCGGIPOSSILSTL 840  
 841 LCSLCYGDMEWKLFAGIRRDGLLJRLVDDFLVTPHLTHAKTFLRLYRGVPBYGCVN L 900  
 841 LCSLCYGDMEWKLFAGIRRDGLLJRLVDDFLVTPHLTHAKTFLRLYRGVPBYGCVN L 900  
 901 RKTIVNPFVDEALGGTAFQMPAHGLPFMCGLLIDTRTLEQVDSYSSARTSSTRASLTF 960  
 901 RKTIVNPFVDEALGGTAFQMPAHGLPFMCGLLIDTRTLEQVDSYSSARTSSTRASLTF 960  
 961 NRGFKAGRMRRKLFQVLRKCHSLFLDQVNSLQTVCNTNIKILLQAYRHFACVLQLP 1020  
 961 NRGFKAGRMRRKLFQVLRKCHSLFLDQVNSLQTVCNTNIKILLQAYRHFACVLQLP 1020  
 1021 FHQQWKNPPTFLRV1SDASLCSYKILKARNAGNMSLGAAGGPLSEAQNLCQAFLL 1080  
 1021 FHQQWKNPPTFLRV1SDASLCSYKILKARNAGNMSLGAAGGPLSEAQNLCQAFLL 1080  
 1081 KLTREHRTVYVPLGSLRLTAOTQLSRKLPSTTLEAANPALPSDFKTLID 1132  
 1081 KLTREHRTVYVPLGSLRLTAOTQLSRKLPSTTLEAANPALPSDFKTLID 1132  
 121 SYLINTVTDALRGSGANCLLJRRGDDVYLHARCAFLVLAFCGFALLDARGGPEAFTTSV 120  
 121 SYLINTVTDALRGSGANCLLJRRGDDVYLHARCAFLVLAFCGFALLDARGGPEAFTTSV 120  
 181 ATQARPPPHASGPERRRLGCRGAAWHSYREAGVPLGLPAGARRGGSAARSLSLPKRRR 240  
 181 ATQARPPPHASGPERRRLGCRGAAWHSYREAGVPLGLPAGARRGGSAARSLSLPKRRR 240

RESULT 9  
 US-10-054-611-225

; Sequence 225 , Application US/10054611  
 ; Publication No. US20030059787A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cech, Thomas R.  
 ; Lingner, Joachim  
 ; Nakamura, Toru  
 ; Chapman, Karen B.  
 ; Morin, Gregg B.  
 ; Harley, Calvin B.  
 ; Andrews, William H.  
 ; ADDRESS: No. US20030059787A1el Telomerase  
 ; NUMBER OF SEQUENCES: 225  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, 8th Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States of America  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: PC-DO/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0 , Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US 10/054,611  
 ; FILING DATE: 18-Jan-2002  
 ; CLASSIFICATION: 536  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/854,050  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: US 08/846,017  
 ; FILING DATE: 25-APR-1997  
 ; APPLICATION NUMBER: US 08/844,419  
 ; FILING DATE: 18-APR-1997  
 ; APPLICATION NUMBER: US 08/724,643  
 ; FILING DATE: 01-OCT-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Apple, Randolph T.  
 ; REGISTRATION NUMBER: 16,429  
 ; PREFERENCE/DOCKET NUMBER: 015389-002930US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; INFORMATION FOR SEQ ID NO: 225:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1132 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 225:  
 ; US-10-054-611-225  
 ; Query Match Score 5961; DB 14; Length 1132;  
 ; Best Local Similarity 100.0%; Pred. No. 0;  
 ; Matches 1132; Conservative 0; Indels 0; Gaps 0;  
 ; QY 1 MPRAPRCAEVRSILRSHYREVPLATEVRLGSPQGWLVQRDPAFRLVAQCLVCVPW 60  
 ; Db 1 MPRAPRCAEVRSILRSHYREVPLATEVRLGSPQGWLVQRDPAFRLVAQCLVCVPW 60  
 ; QY 61 DARPPAAPSFRQVSCLKEVLRVQLCERGAKNVLAFCGFALLDARGGPEAFTTSV 120  
 ; Db 61 DARPPAAPSFRQVSCLKEVLRVQLCERGAKNVLAFCGFALLDARGGPEAFTTSV 120  
 ; QY 121 SYLINTVTDALRGSGANCLLJRRGDDVYLHARCAFLVLAFCGFALLDARGGPEAFTTSV 120  
 ; Db 121 SYLINTVTDALRGSGANCLLJRRGDDVYLHARCAFLVLAFCGFALLDARGGPEAFTTSV 120  
 ; QY 181 ATQARPPPHASGPERRRLGCRGAAWHSYREAGVPLGLPAGARRGGSAARSLSLPKRRR 240  
 ; Db 181 ATQARPPPHASGPERRRLGCRGAAWHSYREAGVPLGLPAGARRGGSAARSLSLPKRRR 240

SEQUENCE LISTING	
-10-105-963-2	
Sequence 1	Application US/10105963
Publication No. US20030058818A1	GENERAL INFORMATION:
APPLICANT: Geron Corporation	APPLICANT: Geron Corporation
APPLICANT: Denning, Chris	APPLICANT: Denning, Chris
APPLICANT: Clark, A. John	APPLICANT: Clark, A. John
APPLICANT: Schiff, J. Michael	APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Transplantation and a Carbohydrate Determinant Selectin	TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Transplantation and a Carbohydrate Determinant Selectin
RESULT 10	RESULT 10
241 GAAPERTPVGCGSSWAHGRTRGPSPDRGFCVYSPARPAEATSSLEGALSGTRSHPSVG 300	241 GAAPERTPVGCGSSWAHGRTRGPSPDRGFCVYSPARPAEATSSLEGALSGTRSHPSVG 300
301 ROHAGGPSTSRRPPRMDTPCPVYAAETKHELYSSGDKEQLRPSFLLSSIRPSLTGARBL 360	301 ROHAGGPSTSRRPPRMDTPCPVYAAETKHELYSSGDKEQLRPSFLLSSIRPSLTGARBL 360
361 VETIFLGRPWPMPGTPLLRLPRLPRLPQYWMQRPLFLLGNAQCPYGVLLKTHCPRLRAVT 420	361 VETIFLGRPWPMPGTPLLRLPRLPQYWMQRPLFLLGNAQCPYGVLLKTHCPRLRAVT 420
421 PAGVCAREKPKQGSSVAAPPEEIDTPRLVQQLRQHSSPQVYGVRACLRLVYGPGLWGS 480	421 PAGVCAREKPKQGSSVAAPPEEIDTPRLVQQLRQHSSPQVYGVRACLRLVYGPGLWGS 480
481 RHNERFLRNLNTKKFISLGKHAKLSSLQELTWKMSVYDCAWLRSPGVCYPAAEHRLREBT 540	481 RHNERFLRNLNTKKFISLGKHAKLSSLQELTWKMSVYDCAWLRSPGVCYPAAEHRLREBT 540
541 LAKPLHLMSVTYVLLSSFFYTTETTFQKNRLPFYRKSVWSKLQSIGTRQHLKRVQRE 600	541 LAKPLHLMSVTYVLLSSFFYTTETTFQKNRLPFYRKSVWSKLQSIGTRQHLKRVQRE 600
601 LSEAEVROHREARPAALLTSRLRFLPKPDGLRPTVMDYVVGARTFRREKRAELTSRYKA 660	601 LSEAEVROHREARPAALLTSRLRFLPKPDGLRPTVMDYVVGARTFRREKRAELTSRYKA 660
661 LPSVLYNBRARRGCLGASVGLDDIIRHAWRTEFVLRVAQDPPBPELYFKVDTGAYDTI 720	661 LPSVLYNBRARRGCLGASVGLDDIIRHAWRTEFVLRVAQDPPBPELYFKVDTGAYDTI 720
721 PDRLTEVIASIIKPKQNTYCVRRYAVOKAAGHIVRKAFKSHVSTLTDLQPYMRQFVAHL 780	721 PDRLTEVIASIIKPKQNTYCVRRYAVOKAAGHIVRKAFKSHVSTLTDLQPYMRQFVAHL 780
781 QETSPLRDAVVIROSSLNEASSGFLFDYFLRMECHAVIRGKSYVOCOGIPQGSILSTL 840	781 QETSPLRDAVVIROSSLNEASSGFLFDYFLRMECHAVIRGKSYVOCOGIPQGSILSTL 840
841 LCSLGMDMENKLFGAICIRDGLLRLVDFELYTPLHTAKTFELRTLVRGYPEPGCVNL 900	841 LCSLGMDMENKLFGAICIRDGLLRLVDFELYTPLHTAKTFELRTLVRGYPEPGCVNL 900
901 RKTVVNFVPEDEALGTAEVQMPAHGLFPWCGLQLLDTRTLEQSDYSSYARTSTRASLT 960	901 RKTVVNFVPEDEALGTAEVQMPAHGLFPWCGLQLLDTRTLEQSDYSSYARTSTRASLT 960
961 NRQFKAGNMRRLKFGVRLRKCHSLFLDQVNSLQTVCTNIIYKILLQAYRFHACVQLQP 1020	961 NRQFKAGNMRRLKFGVRLRKCHSLFLDQVNSLQTVCTNIIYKILLQAYRFHACVQLQP 1020
1021 FHQWKNPFTFELRVIDTASILCYSILKAKNAGMSLGKGAAGPLPSEAVQWLQHQAFL 1080	1021 FHQWKNPFTFELRVIDTASILCYSILKAKNAGMSLGKGAAGPLPSEAVQWLQHQAFL 1080
1081 KLTTRHRTVYPLIGSLRATQTSRKLPGTTLTALEAANPALPSDFKTLID 1132	1081 KLTTRHRTVYPLIGSLRATQTSRKLPGTTLTALEAANPALPSDFKTLID 1132
1081 KLTTRHRTVYPLIGSLRATQTSRKLPGTTLTALEAANPALPSDFKTLID 1132	1081 KLTTRHRTVYPLIGSLRATQTSRKLPGTTLTALEAANPALPSDFKTLID 1132

Qy 841 LCSLCYGDMENTLFAIGIRRDGLLRLVDDFLVTPHILTHAKTFLRTLVRGVPEYCCVNL 900  
 Db 841 LCSLCYGDMENTLFAIGIRRDGLLRLVDDFLVTPHILTHAKTFLRTLVRGVPEYCCVNL 900  
 Qy 901 RKTIVNFPVEDBALGGTAFVOMPAHGLFPWCGLLDDTLEQVSDYSYARTSIRASLTF 960  
 Db 901 RKTIVNFPVEDBALGGTAFVOMPAHGLFPWCGLLDDTLEQVSDYSYARTSIRASLTF 960  
 Qy 961 NRGFKAGRNMRKLFGYLRLKCHSLETDLOVNSLOTYCNYKILLQAYTRFHACVQLP 1020  
 Db 961 NRGFKAGRNMRKLFGYLRLKCHSLETDLOVNSLOTYCNYKILLQAYTRFHACVQLP 1020  
 Qy 1021 FHQQVWNKPTPFLRVISDTASLCYSTIKAKNAGMSLGAKGAAGPLPSEAVQWLQAFEL 1080  
 Db 1021 FHQQVWNKPTPFLRVISDTASLCYSTIKAKNAGMSLGAKGAAGPLPSEAVQWLQAFEL 1080  
 Qy 1081 KLTTRHRYTYVPLGSLRTAQTLQRSLKPGTTLTALEAANPALPDKFTLD 1132  
 Db 1081 KLTTRHRYTYVPLGSLRTAQTLQRSLKPGTTLTALEAANPALPDKFTLD 1132

RESULT 11  
 US 10-044-692-2  
 Sequence 2, Application US/10444692  
 Publication No. US2003009634A1  
 GENERAL INFORMATION:  
 APPLICANT: Cech, Thomas R.  
 Lingner, Joachim  
 Nakamura, Toru  
 Chapman, Karen B.  
 Morin, Gregg B.  
 Harley, Calvin  
 Andrews, William H.  
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS  
 NUMBER OF SEQUENCES: 335  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, 8th Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States of America  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US 10/044,692  
 PILING DATE: 11-Jan-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/912, 951  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: US 08/854, 050  
 FILING DATE: 09-MAY-1997  
 APPLICATION NUMBER: US 08/851, 843  
 FILING DATE: 06-MAY-1997  
 APPLICATION NUMBER: US 08/846, 017  
 FILING DATE: 25-APR-1997  
 APPLICATION NUMBER: US 08/844, 419  
 FILING DATE: 18-APR-1997  
 APPLICATION NUMBER: US 08/724, 643  
 FILING DATE: 01-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Apple, Randolph T.  
 REGISTRATION NUMBER: 36, 429  
 REFERENCE/DOCKET NUMBER: 015389-002600US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-044-692-2  
 Query Match 100.0%; Score 5961; DB 14; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0; Gaps 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MPRPRCRAVRSLSRSHREVLPLATFVRLGPQWRVLVQRGDPAAFLVAQCLVCPW 60  
 Db 1 MPRPRCRAVRSLSRSHREVLPLATFVRLGPQWRVLVQRGDPAAFLVAQCLVCPW 60  
 Qy 61 DARPPPAAFSFRQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPFAFTSVR 120  
 Db 61 DARPPPAAFSFRQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPFAFTSVR 120  
 Qy 121 SYLPNTVTDALRGSGANGHLLPRVGDVLUHLJARCAFLVJYAPSCAYQVCCBPPLQIGA 180  
 Db 121 SYLPNTVTDALRGSGANGHLLPRVGDVLUHLJARCAFLVJYAPSCAYQVCCBPPLQIGA 180  
 Qy 181 ATQRPPPHASGPRRLGCERAWNHSREAGYPLGLPAPGARRGGSASRSLPLPKPRR 240  
 Db 181 ATQRPPPHASGPRRLGCERAWNHSREAGYPLGLPAPGARRGGSASRSLPLPKPRR 240  
 Qy 241 GAAEPEPTPGQGSSWAHPGRTRGPSDRGFCVVSPARPAAEATSLLEGALSCTRSHPSVG 300  
 Db 241 GAAEPEPTPGQGSSWAHPGRTRGPSDRGFCVVSPARPAAEATSLLEGALSCTRSHPSVG 300  
 Qy 301 RQHAGPPSTSRPBPNDTPCPPEVYAAETKHFELYSQGDKEQLRSPFJLSSLRPSLTGARRL 360  
 Db 301 RQHAGPPSTSRPBPNDTPCPPEVYAAETKHFELYSQGDKEQLRSPFJLSSLRSLTGARRL 360  
 Qy 361 VETFLGSRPMMDGTPLRPLPQRQYQWQMRPLFELJGNHACQPGVILKTHCPLRAYT 420  
 Db 361 VETFLGSRPMMDGTPLRPLPQRQYQWQMRPLFELJGNHACQPGVILKTHCPLRAYT 420  
 Qy 421 PAAGVCAKREPKQGSSVAAPBEEEDTPRRLVQLRQHSSSWQYGFVACLRRLVPGLGWS 480  
 Db 421 PAAGVCAKREPKQGSSVAAPBEEEDTPRRLVQLRQHSSSWQYGFVACLRRLVPGLGWS 480  
 Qy 481 RINERRFLRNTKCFISLGKHAKLSQLDTWMSVRCDAWLRSRSPGVGCPVPAAEHRLREEI 540  
 Db 481 RINERRFLRNTKCFISLGKHAKLSQLDTWMSVRCDAWLRSRSPGVGCPVPAEHLRLBEI 540  
 Qy 541 LAKFLHNMMSVYVLLRSFPTVETTFQKQRLFYYKSVWSKLOSTGIRQHLKRVOLRE 600  
 Db 541 LAKFLHNMMSVYVLLRSFPTVETTFQKQRLFYYKSVWSKLOSTGIRQHLKRVOLRE 600  
 Qy 601 LSEAEVQHREARPALLTSRFLPKDGLRPIKPDGLRPIVNMDDYVGARTFREKRAEPLTSRVKA 660  
 Db 601 LSEAEVQHREARPALLTSRFLPKDGLRPIVNMDDYVGARTFREKRAEPLTSRVKA 660  
 Qy 661 LFSVLYNERARRPGLGASVLGDDIHTHAWRFLVRLYRAODPPPELYFKVUDVGTAYDTI 720  
 Db 661 LFSVLYNERARRPGLGASVLGDDIHTHAWRFLVRLYRAODPPPELYFKVUDVGTAYDTI 720  
 Qy 721 PODRLTEVIASTIKPONTYCVRAYVQKAAGHWRKAFKSHVSTLTDLQPYMROQYV AHL 780  
 Db 721 PODRLTEVIASTIKPONTYCVRAYVQKAAGHWRKAFKSHVSTLTDLQPYMROQYV AHL 780  
 Qy 781 QETSPLEDAVIVFQSSSLNEASSGLFDVFLRMCIIHARVIGSKSYVQCG1PQGS1SLSTL 840  
 Db 781 QETSPLEDAVIVFQSSSLNEASSGLFDVFLRMCIIHARVIGSKSYVQCG1PQGS1SLSTL 840  
 Qy 841 LCSLCYGDMENTLFAIGIRRDGLLRLVDDFLVTPHILTHAKTFLRTLVRGVPEYCCVNL 900  
 Db 841 LCSLCYGDMENTLFAIGIRRDGLLRLVDDFLVTPHILTHAKTFLRTLVRGVPEYCCVNL 900  
 Qy 901 RKTIVNFPVEDALGGTAFVQMPANGLFPWCCLLDTLRTLEVQSDYSSYARTSIRASLTF 960

RESULT 12  
US-10-044-519-2

Sequence 2, Application US/10044519

Publication No. US20030100093A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Moin, Gregg B.  
Harley, Calvin  
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/044,519  
FILING DATE: 11-Jan-2002  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/912,951  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1132 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-044-539-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Index 0; Gaps 0;

Qy 1 MPRAPCRAYRSLSLRSHYREVLPATFVRQLGPQGMWLVORGDPAAFRALVAQCLVCVPW 60  
Db 1 MPRAPCRAYRSLSLRSHYREVLPATFVRQLGPQGMWLVORGDPAAFRALVAQCLVCVPW 60

Qy 61 DARPPAAPSFRQVSCSKELVARTVQLCERGAKVNLAFQGFLDARGGPEAFITSVR 120  
Db 61 DARPPAAPSFRQVSCSKELVARTVQLCERGAKVNLAFQGFLDARGGPEAFITSVR 120

Qy 121 SYLPNTVTDALRGSGAWGLLRLRVEDDVYLHLARCALFVLPVSCAYQVCGPPIYQQLGA 180  
Db 121 SYLPNTVTDALRGSGAWGLLRLRVEDDVYLHLARCALFVLPVSCAYQVCGPPIYQQLGA 180

Qy 181 ATQARPPHASGPRLGCRAMWHSVREAGVPLGPAPGARRGGASRSLPLPKRPRR 240  
Db 181 ATQARPPHASGPRLGCRAMWHSVREAGVPLGPAPGARRGGASRSLPLPKRPRR 240

Qy 241 GAAPEPERTPVQGSWAHPGRTGSDRGCVSPARPABEATLSEGALSGTRSHPSVG 300  
Db 241 GAAPEPERTPVQGSWAHPGRTGSDRGCVSPARPABEATLSEGALSGTRSHPSVG 300

Qy 301 RQHAGGPPPSRSPRPPWDITCPPPYTAETKHFLLYSGDKEOLRPSFLLSSURPSLTGARRL 360  
Db 301 RQHAGGPPPSRSPRPPWDITCPPPYTAETKHFLLYSGDKEOLRPSFLLSSURPSLTGARRL 360

Qy 361 VETIFIGSRPWPMPGPRRLPRLPQWQMRPLFLIGLNAQCPYGVLLKTHCPLRAAVT 420  
Db 361 VETIFIGSRPWPMPGPRRLPRLPQWQMRPLFLIGLNAQCPYGVLLKTHCPLRAAVT 420

Qy 421 PAAGYCAREKPGQSYVAAPEEEEDTDPRLVQOLLQHSSPQWQYGFYTRACLRLVPPLGWS 480  
Db 421 PAAGYCAREKPGQSYVAAPEEEEDTDPRLVQOLLQHSSPQWQYGFYTRACLRLVPPLGWS 480

Qy 481 RHNERFRFLRTRKKFISLGKHAKLSQLQELTWMRSVDCAWJRSRPSGVGCYAAEHRLREI 540  
Db 481 RHNERFRFLRTRKKFISLGKHAKLSQLQELTWMRSVDCAWJRSRPSGVGCYAAEHRLREI 540

Qy 541 LAKFELHMLMSVYVWLLRSFPTETTFRQNLFFYRKSTWKLQSIGIRQLHKLKVQLRE 600  
Db 541 LAKFELHMLMSVYVWLLRSFPTETTFRQNLFFYRKSTWKLQSIGIRQLHKLKVQLRE 600

Qy 601 LSEAEVQHREARPALLTSRLRFIPKPDGLRPIVNMYYVQGARTPRREKAERLTSRVKA 660  
Db 601 LSEAEVQHREARPALLTSRLRFIPKPDGLRPIVNMYYVQGARTPRREKAERLTSRVKA 660

Qy 661 LFSVINYERARRPGLGASVGLDDLHRAVRTFVLRVRAODPPPELYFVKVDVTGAYDTI 720  
Db 661 LFSVINYERARRPGLGASVGLDDLHRAVRTFVLRVRAODPPPELYFVKVDVTGAYDTI 720

Qy 721 PQDRLETEVIAISIUKQNTCYRRAVYOKAAGHIVRKAFKSHVSTLTDQPYMRFQV AHL 780  
Db 721 PQDRLETEVIAISIUKQNTCYRRAVYOKAAGHIVRKAFKSHVSTLTDQPYMRFQV AHL 780

Qy 781 QETSPLRDAVWVTEQSSLNFAASGLDFVFLRFMCHAVTRGKSTVQCGQIPQGSILSTL 840  
Db 781 QETSPLRDAVWVTEQSSLNFAASGLDFVFLRFMCHAVTRGKSTVQCGQIPQGSILSTL 840

Qy 841 LCSLCYGDMEKLFAGIRDRGLLRLVDDFLYVTPHLTHAKTFRTLYVQPEYGCYVNL 900  
Db 841 LCSLCYGDMEKLFAGIRDRGLLRLVDDFLYVTPHLTHAKTFRTLYVQPEYGCYVNL 900

Qy 901 RKTIVNFPVDEALGCTAQMAGLFPNCGLLDTRTEQSDYSSYARTSIRASLTTF 960  
Db 901 RKTIVNFPVDEALGCTAQMAGLFPNCGLLDTRTEQSDYSSYARTSIRASLTTF 960

Qy 961 NRGFKAGRNNRKLFEVRLKCHSLFLDLOVNSLQFTCINYKLLQAYRFHACVQLQP 1020

Db 961 NRGFKAGNMRKLFGLVRLKCHSLFIDLQVNSLQTVCTNIYKILLQAYRFHACVILQLP 1020  
 Qy 1021 FHOQWKNPTEFLRVTSIDTLCYTSILAKNAGMSLGAKGAAGPLPSEAQWLCQAFLL 1080  
 Db 1021 FHQQWKNPTEFLRVTSIDTLCYTSILAKNAGMSLGAKGAAGPLPSEAQWLCQAFLL 1080  
 Qy 1081 KLTRHRTYVPLGSLRTAQQLSRKLPGTTLTALEAANPALPSDFKTLID 1132  
 Db 1081 KLTRHRTYVPLGSLRTAQQLSRKLPGTTLTALEAANPALPSDFKTLID 1132

RESULT 13  
 US-10-295-681-57  
 ; Sequence 57, Application US/10295681  
 ; Publication No. US2003016622/0A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: E. Premkumar Reddy  
 ; APPLICANT: Sushil G. Rane  
 ; APPLICANT: Richard V. Metru  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REVERSIBLY  
 ; INDUCING CONTINUAL GROWTH IN NORMAL CELLS  
 ; FILE REFERENCE: 6056-307  
 ; CURRENT APPLICATION NUMBER: US/10/295, 681  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/334, 760  
 ; PRIOR FILING DATE: 2001-11-15  
 ; NUMBER OF SEQ ID NO: 69  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 57  
 ; LENGTH: 1132  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-295-681-57

Query Match 100.0%; Score 5961; DB 14; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gads 0;  
 Matches 1132; Conservative 0; ;

Qy 1 MPRAPCRAYRSLLSHYREVLPLATFVRRLQPGQWRLYORGDPAAFRALVAQCLVCEW 60  
 Db 1 MPRAPCRAYRSLLSHYREVLPLATFVRRLQPGQWRLYORGDPAAFRALVAQCLVCEW 60

Qy 61 DARPPAAPSFRQVSKELKLYVQLRCERGAKVLAFGPAFLDARGGPPEAFTTSVYR 120  
 Db 61 DARPPAAPSFRQVSKELKLYVQLRCERGAKVLAFGPAFLDARGGPPEAFTTSVYR 120

Qy 121 SYLPNTVTDALRGSAWGLLRLRVDVLLARCAFLVADSCAYQVCGPPLYQJGA 180  
 Db 121 SYLPNTVTDALRGSAWGLLRLRVDVLLARCAFLVADSCAYQVCGPPLYQJGA 180

Qy 181 ATQARPPPHASGPRLGCBAWNHSVREAGVPLGSLPAPGARRGGASRSPLPKRPR 240  
 Db 181 ATQARPPPHASGPRLGCBAWNHSVREAGVPLGSLPAPGARRGGASRSPLPKRPR 240

Qy 241 GAAPEPRTPVGQSWHPGRTRGSPDSRGFCVSPARAEATSLLEGALSCTRHSHPSYG 300  
 Db 241 GAAPEPRTPVGQSWHPGRTRGSPDSRGFCVSPARAEATSLLEGALSCTRHSHPSYG 300

Qy 361 VETIFLGSRPMPGPTRPLPRLPQRYWQMRPLFIELGNGHAQCPYGVLLKTHCPRLRAVT 420  
 Db 361 VETIFLGSRPMPGPTRPLPRLPQRYWQMRPLFIELGNGHAQCPYGVLLKTHCPRLRAVT 420

Qy 421 PAAGYCAREPKQGSTAAPEEBDTDPRRLYQOLRHOHSPQVYGFVACLRLVYPPGJMG 480  
 Db 421 PAAGYCAREPKQGSTAAPEEBDTDPRRLYQOLRHOHSPQVYGFVACLRLVYPPGJMG 480

Qy 481 RHNERFLRNTKCF1SLGHAKLSQLQELTWKMSYRDCAMLRSPGVCYCPAAEHLRLREB 540  
 Db 481 RHNERFLRNTKCF1SLGHAKLSQLQELTWKMSYRDCAMLRSPGVCYCPAAEHLRLREB 540

Qy 541 LAKEFLHWMVSYYVELLRSFFYYTTETTFOKNRLFYRKSVWSKLQSIGTROHLKRVOLRE 600  
 Db 541 LAKEFLHWMVSYYVELLRSFFYYTTETTFOKNRLFYRKSVWSKLQSIGTROHLKRVOLRE 600  
 Qy 601 LSEAEVROHREARPALLTSRLRFPKPDLRPTVNMDDYVGARTFRERKERAERTSRSVKA 660  
 Db 601 LSEAEVROHREARPALLTSRLRFPKPDLRPTVNMDDYVGARTFRERKERAERTSRSVKA 660  
 Qy 661 LFSVLYNBERARRPOLLGASVGLGIDDIHAWRTVFLVRAQDPPELYFVKVDTGAYDTI 720  
 Db 661 LFSVLYNBERARRPOLLGASVGLGIDDIHAWRTVFLVRAQDPPELYFVKVDTGAYDTI 720  
 Qy 721 PQDLTEVIASIKPQNTYCVRYYAVVOKAAHGHVRKAFKSHVSTLTDLQPMRQYVH 780  
 Db 721 PQDLTEVIASIKPQNTYCVRYYAVVOKAAHGHVRKAFKSHVSTLTDLQPMRQYVH 780  
 Qy 781 QETSPRLDAVVIQESSLNEASSGLFDVFLRMCHHAVRIGKSYVOCQGIPQGSILSTL 840  
 Db 781 QETSPRLDAVVIQESSLNEASSGLFDVFLRMCHHAVRIGKSYVOCQGIPQGSILSTL 840  
 Qy 841 LCSLCYGDMEKULEAGIIRDGLLRLVDFDLYVTPHILTHAKTFLRTLVGVPBYGVNL 900  
 Db 841 LCSLCYGDMEKULEAGIIRDGLLRLVDFDLYVTPHILTHAKTFLRTLVGVPBYGVNL 900  
 Qy 901 RKTVNPNPVDEALGGTAFVQMPAHLFPWCGLUDLTLEQSDYSSARTSTRASLT 960  
 Db 901 RKTVNPNPVDEALGGTAFVQMPAHLFPWCGLUDLTLEQSDYSSARTSTRASLT 960  
 Qy 961 NRGFKAQRNMRKLFGVLRKCHSLFLDLQVNSLQTYCTNIVKILLQAYRFHACVILQLP 1020  
 Db 961 NRGFKAQRNMRKLFGVLRKCHSLFLDLQVNSLQTYCTNIVKILLQAYRFHACVILQLP 1020  
 Qy 1081 KLTJHRVTVPLIGSLRTAQTSRKLPGTTLTALEAANPALPSDFKTLID 1132  
 Db 1081 KLTJHRVTVPLIGSLRTAQTSRKLPGTTLTALEAANPALPSDFKTLID 1132  
 RESULT 14  
 US-10-295-681-57  
 ; Sequence 2, Application US/10325810  
 ; Publication No. US20030204069A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cech, Thomas R.  
 ; APPLICANT: Lingner, Joachim  
 ; APPLICANT: Nakamura, Toru  
 ; APPLICANT: Chapman, Karen B.  
 ; APPLICANT: Morin, Gregg B.  
 ; APPLICANT: Andrews, William H.  
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
 ; NUMBER OF SEQUENCES: 633  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/325, 810  
 ; FILING DATE: 20-Dec-2002  
 ; CLASSIFICATION: <Unknown>  
 ; PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181  
 FILING DATE: 29-Sep-1997  
 APPLICATION NUMBER: US 08/724,643  
 FILING DATE: 01-OCT-1996  
 APPLICATION NUMBER: US 08/844,419  
 FILING DATE: 18-APR-1997  
 APPLICATION NUMBER: US 08/846,017  
 FILING DATE: 25-APR-1997  
 APPLICATION NUMBER: US 08/851,843  
 FILING DATE: 06-MAY-1997  
 APPLICATION NUMBER: US 08/854,050  
 FILING DATE: 09-MAY-1997  
 APPLICATION NUMBER: US 08/911,312  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: US 08/912,951  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: US 08/915,503  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: WO PCT/US97/17885  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Auerhuis, Scott L.  
 REGISTRATION NUMBER: 42,271  
 REFERENCE/DOCKET NUMBER: 015389-002620US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 MOLECULE TYPE: protein  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-325-810-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; N mismatches 0;  
 Indels 0; Gaps 0;

QY 1 MPRAPCRAYSLRSHREVPLATEFVRRLGPQGMWLVQRGDPAAFRALVAQCLVCPW 60  
 DB 1 MPRAPCRAYSLRSHREVPLATEFVRRLGPQGMWLVQRGDPAAFRALVAQCLVCPW 60

QY 61 DARPPAAPSAPSPRQVSLKELYKARVQLCERGAKNVLAFGALLDARGGPPEAFTSVR 120  
 DB 61 DARPPAAPSAPRQVSLKELYKARVQLCERGAKNVLAFGALLDARGGPPEAFTSVR 120

QY 121 SYLPNTVTDAIRSGAWGLLRLRVGDDVLHLLARCAFLVAPSCAYQCGPPLYQLGA 180  
 DB 121 SYLPNTVTDAIRSGAWGLLRLRVGDDVLHLLARCAFLVAPSCAYQCGPPLYQLGA 180

QY 181 ATQARPYPHASGPRRLGCERAWNHSVREAGVPLGPAPGARRGGASRSPLPKPRRR 240  
 DB 181 ATQARPYPHASGPRRLGCERAWNHSVREAGVPLGPAPGARRGGASRSPLPKPRRR 240

QY 241 GAAPEPRTPYGOGSVAHPGPTRGSDRGFCVVSAPABEATSLGALSGTRISHPSVG 300  
 DB 241 GAAPEPRTPYGOGSVAHPGPTRGSDRGFCVVSAPABEATSLGALSGTRISHPSVG 300

QY 301 RQHHAGPSPSTSRRPPWDTCPPTVYTAETKHFYSSCDKEQLRSPFLSSLRPSLTGARRL 360  
 DB 301 RQHHAGPSPSTSRRPPWDTCPPTVYTAETKHFYSSCDKEQLRSPFLSSLRPSLTGARRL 360

QY 361 VETIFGSRPMGPPTPRPLPRLPQRYWQMPFLFILELGNHAQCPYGVLLKTHCPLRAVTT 420  
 DB 361 VETIFGSRPMGPPTPRPLPRLPQRYWQMPFLFILELGNHAQCPYGVLLKTHCPLRAVTT 420

QY 421 PAAGVCAREKEQGSTAAYAEEEDDTDPRLVQLRQHSSPWQVYGFTRACRLRVLPGWLGS 480  
 DB 421 PAAGVCAREKEQGSTAAYAEEEDDTDPRLVQLRQHSSPWQVYGFTRACRLRVLPGWLGS 480

QY 481 RHNERFLRNTKKFISLGHAKLSQLBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Db 481 RHNERFLRNTKKFISLGHAKLSQLBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy 541 LAKFHWMNSVYVYELLRSPFVYETTFFKQNLFLPYKRSWKSQSIGTRQHLRQVLR 600  
 Db 541 LAKFHWMNSVYVYELLRSPFVYETTFFKQNLFLPYKRSWKSQSIGTRQHLRQVLR 600

Qy 601 LSEAEVROREARAPALLTSRLRF1PKPDGLRSPITNMDDYVUGARTFRREKERAERTSRVKA 660  
 Db 601 LSEAEVROREARAPALLTSRLRF1PKPDGLRSPITNMDDYVUGARTFRREKERAERTSRVKA 660

Qy 661 LPSLNLVERARRPGLGASVGLGDDIHRARWFYLRVRAQDPPELYFVYDVTGAYDTI 720  
 Db 661 LPSLNLVERARRPGLGASVGLGDDIHRARWFYLRVRAQDPPELYFVYDVTGAYDTI 720

Qy 721 PQDRTEVIASTIIPQNTCVRRAVVKQAAHGHVRKAPSKHVSHTLTDIOPYMQFVAHL 780  
 Db 721 PQDRTEVIASTIIPQNTCVRRAVVKQAAHGHVRKAPSKHVSHTLTDIOPYMQFVAHL 780

Qy 781 QETSPRLDAVIEQSSSLANBASSGLPFDVLFREMCHAVIRGKSYVQCGQIPQGSILSTL 840  
 Db 781 QETSPRLDAVIEQSSSLNEASSGLFDVFLRFMCHAVIRGKSYVQCGQIPQGSILSTL 840

Qy 841 LCLSCYGDMEALKLPAIGIRDGLLRLVDDFLVTPHFLAKTFRTLVRGVPEIGCVVNL 900  
 Db 841 LCLSCYGDMEALKLPAIGIRDGLLRLVDDFLVTPHFLAKTFRTLVRGVPEIGCVVNL 900

Qy 901 RKTVNFPYDEAUGTAFVQMPAGLFPMCGLLIDTRLEVQSDYSSSTARTSRSATLTF 960  
 Db 901 RKTVNFPYDEAUGTAFVQMPAGLFPMCGLLIDTRLEVQSDYSSSTARTSRSATLTF 960

Qy 961 NRGFKAQRNMRRKUFLKGVLRLKCHSLFDLQVNSLQTVCTNIYKLLQAYRFHACVLQLP 1020  
 Db 961 NRGPZAGRNMRRKUFLKGVLRLKCHSLFDLQVNSLQTVCTNIYKLLQAYRFHACVLQLP 1020

Qy 1021 FHQQWKNPFTFLVVISDASLCLYSILKAKNAGNSLGAAGGLPSEAVQWLQHQAFLL 1080  
 Db 1021 FHQQWKNPFTFLVVISDASLCLYSILKAKNAGNSLGAAGGLPSEAVQWLQHQAFLL 1080

Qy 1081 KLTRHRVTVPLQGSLSLRTQTOUSRLPGTTLTAAEAANPALSDFKTLID 1132  
 Db 1081 KLTRHRVTVPLQGSLSLRTQTOUSRLPGTTLTAAEAANPALSDFKTLID 1132

RESULT 15

US-10-388-578-2  
 ; Sequence 2, Application US/10388578  
 ; Publication No. US2003022411A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; ATTORNEY: Stanton, Lawrence  
 ; ATTORNEY: Ralph, Brandenberger  
 ; ATTORNEY: Joseph, Gold D.  
 ; ATTORNEY: John, Irving  
 ; ATTORNEY: Mandalam, Ramkumar  
 ; ATTORNEY: Mok, Michael  
 ; ATTORNEY: Michael, Michael  
 ; ATTORNEY: Shelton, Dawne  
 ; TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of Hematopoietic Stem Cells  
 ; FILE REFERENCE: 135/001  
 ; CURRENT APPLICATION NUMBER: US/10/388,578  
 ; CURRENT FILING DATE: 2003-03-13  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: Custom  
 ; SEQ ID NO: 2  
 ; LENGTH: 1132  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-388-578-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; N mismatches 0;  
 Indels 0; Gaps 0;

QY 1 MPRAPCRAYSLRSHREVPLATEFVRRLGPQGMWLVQRGDPAAFRALVAQCLVCPW 60  
 DB 1 MPRAPCRAYSLRSHREVPLATEFVRRLGPQGMWLVQRGDPAAFRALVAQCLVCPW 60

QY 61 DARPPAAPSAPRQVSLKELYKARVQLCERGAKNVLAFGALLDARGGPPEAFTSVR 120  
 DB 61 DARPPAAPSAPRQVSLKELYKARVQLCERGAKNVLAFGALLDARGGPPEAFTSVR 120

QY 121 SYLPNTVTDAIRSGAWGLLRLRVGDDVLHLLARCAFLVAPSCAYQCGPPLYQLGA 180  
 DB 121 SYLPNTVTDAIRSGAWGLLRLRVGDDVLHLLARCAFLVAPSCAYQCGPPLYQLGA 180

QY 181 ATQARPYPHASGPRRLGCERAWNHSVREAGVPLGPAPGARRGGASRSPLPKPRRR 240  
 DB 181 ATQARPYPHASGPRRLGCERAWNHSVREAGVPLGPAPGARRGGASRSPLPKPRRR 240

QY 241 GAAPEPRTPYGOGSVAHPGPTRGSDRGFCVVSAPABEATSLGALSGTRISHPSVG 300  
 DB 241 GAAPEPRTPYGOGSVAHPGPTRGSDRGFCVVSAPABEATSLGALSGTRISHPSVG 300

QY 301 RQHHAGPSPSTSRRPPWDTCPPTVYTAETKHFYSSCDKEQLRSPFLSSLRPSLTGARRL 360  
 DB 301 RQHHAGPSPSTSRRPPWDTCPPTVYTAETKHFYSSCDKEQLRSPFLSSLRPSLTGARRL 360

QY 361 VETIFGSRPMGPPTPRPLPRLPQRYWQMPFLFILELGNHAQCPYGVLLKTHCPLRAVTT 420  
 DB 361 VETIFGSRPMGPPTPRPLPQRYWQMPFLFILELGNHAQCPYGVLLKTHCPLRAVTT 420

QY 421 PAAGVCAREKEQGSTAAYAEEEDDTDPRLVQLRQHSSPWQVYGFTRACRLRVLPGWLGS 480  
 DB 421 PAAGVCAREKEQGSTAAYAEEEDDTDPRLVQLRQHSSPWQVYGFTRACRLRVLPGWLGS 480

QY 481 RHNERFLRNTKKFISLGHAKLSQLBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy	1 MPRAPRCAVRSLRSLRSYREVPLATFVRRLGPQGIVRLVQRGDPAAFRALVAOCLVCVPW	60	Qy	1081 KLTTRHRVTVVPLUGSLRATAQTLSRKUPSTTLTALEAAANPALPSDFKTIID 1132
Db	1 MPRAPRCAVRSLRSLRSYREVPLATFVRRLGPQGIVRLVQRGDPAAFRALVAOCLVCVPW	60	Db	1081 KLTTRHRVTVVPLUGSLRATAQTLSRKUPSTTLTALEAAANPALPSDFKTIID 1132
Qy	61 DARPPPAAPSFROVSCLEKELVARVLQRLCERGAKIVLAFCGFALLDQARGGPEAFTTSYR	120		
Db	61 DARPPPAAPSFROVSCLEKELVARVLQRLCERGAKIVLAFCGFALLDQARGGPEAFTTSYR	120		
Qy	121 SYLPNTVTDALRGSGAWGLLRRVGDDVLLHLLARCAFLVLPASCAYQVCGPFLYQLGA 180			
Db	121 SYLPNTVTDALRGSGAWGLLRRVGDDVLLHLLARCAFLVLPASCAYQVCGPFLYQLGA 180			
Qy	181 ATQARPDPHASPRRIGCEAWNHSREAGVPLGLPAPGARRRGGASRSLPLPKPRR 240			
Db	181 ATQARPDPHASPRRIGCEAWNHSREAGVPLGLPAPGARRRGGASRSLPLPKPRR 240			
Qy	241 GAPEPRTPYCQGSWAHPGRTRGSPDRGFCVVSAPRABEATSLLEGALSGTRSHSPSYG 300			
Db	241 GAPEPRTPYCQGSWAHPGRTRGSPDRGFCVVSAPRABEATSLLEGALSGTRSHSPSYG 300			
Qy	301 RQHHAGPGEPSRPRPWDTCPYPPVYAAETKHFLYSSGDKEQLRSPSLSSLRPSLTGARL 360			
Db	301 RQHHAGPGEPSRPRPWDTCPYPPVYAAETKHFLYSSGDKEQLRSPSLSSLRPSLTGARL 360			
Qy	361 VETIFGSRPRMPCGTPRRLPRLPQLQRYWQMPFLLELLGNEAQCPCVGVLKTHCPLRAVT 420			
Db	361 VETIFGSRPRMPCGTPRRLPRLPQLQRYWQMPFLLELLGNEAQCPCVGVLKTHCPLRAVT 420			
Qy	421 PAAGVCAERKQGSVAAPEEBDTDPRLVQLLROHSSPWQYGFYVACRLRRLVPGJWGS 480			
Db	421 PAAGVCAERKQGSVAAPEEBDTDPRLVQLLROHSSPWQYGFYVACRLRRLVPGJWGS 480			
Qy	481 RHNERFLRNTKTFISLGKAHLSLQELTWSMVRDCANLRSRGCGVCPAAEHLRREBI 540			
Db	481 RHNERFLRNTKTFISLGKAHLSLQELTWSMVRDCANLRSRGCGVCPAAEHLRREBI 540			
Qy	541 LAKFLHWMSTYVVELLRSFPPYVETTEFQKNRLFFYRKSYWWSKLSQISIGTRQHLKRVQRE 600			
Db	541 LAKFLHWMSTYVVELLRSFPPYVETTEFQKNRLFFYRKSYWWSKLSQISIGTRQHLKRVQRE 600			
Qy	601 LSEAETVRQHREARPALTSURFLPKPDKGLRPIVNMDDYVQGARTFRERKRAERLTSYKA 660			
Db	601 LSEAETVRQHREARPALTSURFLPKPDKGLRPIVNMDDYVQGARTFRERKRAERLTSYKA 660			
Qy	661 LFSVINYERARRPGLGASYVGLDDTHRAWTFVLRVQDPPELYFKVDTGAYTI 720			
Db	661 LFSVINYERARRPGLGASYVGLDDTHRAWTFVLRVQDPPELYFKVDTGAYTI 720			
Qy	721 PQRDLTEVATASIIKQNTCYVRRYAVVQKAAGHGVKAFKSHYSTLTDQPMYRQFYHL 780			
Db	721 PQRDLTEVATASIIKQNTCYVRRYAVVQKAAGHGVKAFKSHYSTLTDQPMYRQFYHL 780			
Qy	781 QETSPSLRADVIEQSSSLNEAASSGLFDVLFMCHHARVIGKSYVQCGIPOGSILSTL 840			
Db	781 QETSPSLRADVIEQSSSLNEAASSGLFDVLFMCHHARVIGKSYVQCGIPOGSILSTL 840			
Qy	841 LCSLCYGDMEWKFLAGIIRGGLLRLVDDFLVPHLTHAKTFRLVTRGVPEYGCVNL 900			
Db	841 LCSLCYGDMEWKFLAGIIRGGLLRLVDDFLVPHLTHAKTFRLVTRGVPEYGCVNL 900			
Qy	901 RKTIVNFPYVEDEALGTAIVQMPAHGLFPWCGJLJDDTKLEVSODYSSYARTSIRASITF 960			
Db	901 RKTIVNFPYVEDEALGTAIVQMPAHGLFPWCGJLJDDTKLEVSODYSSYARTSIRASITF 960			
Qy	961 NRGFKAIGNMRRKLFGLVRLKCHSLEFLDQNSLQTYCTNIVKILLQAYRPHACULQLP 1020			
Db	961 NRGFKAIGNMRRKLFGLVRLKCHSLEFLDQNSLQTYCTNIVKILLQAYRPHACULQLP 1020			
Qy	1021 FHQQWKNPFFLVRVISDASLCTSILAKAQNAGNSLGFKAAGPLPSAVQNLCHOQFL 1080			
Db	1021 FHQQWKNPFFLVRVISDASLCTSILAKAQNAGNSLGFKAAGPLPSAVQNLCHOQFL 1080			

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:23:35 ; Search time 50 Seconds  
(without alignments)  
2178.348 Million cell updates/sec

Title: US-10-053-758-225  
Perfect score: 5961  
Sequence: 1 MPRAPCRAVRSILRSHYRE . . . . . TALEAAANPALPSDFKTLID 1132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79/\*  
1: Pirl1/\*  
2: Pirl2/\*  
3: Pirl3/\*  
4: Pirl4/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	5961	100.0	1.132	2	T03844	telomerase catalytic chain - human
2	724.5	12.2	1.123	2	T51517	N; Alternative names: telomerase reverse transcriptase
3	594.5	10.0	0.989	2	T03838	C; Species: Homo sapiens (man)
4	395	6.6	1.132	2	T31107	C; Accession: T03844
5	363	6.1	1.117	2	T14891	R; Nakamura, T.M.; Marin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J. Science 277, 955-959, 1997
6	356.5	6.0	0.884	2	S53396	A; Title: Telomerase catalytic subunit homologs from fission yeast and human.
7	176.5	3.0	3.530	2	A59266	A; Reference number: Z15111; MUID:97400623; PMID:9252327
8	172.5	2.9	0.660	1	Q0BE3	A; Status: preliminary; translated from GB/EMBL/DBJ
9	171.4	2.4	3.511	2	A59295	A; Accession: T03844
10	142.5	2.4	1.560	2	T00080	A; Molecule type: mRNA
11	140.5	2.4	1.892	2	T18314	A; Residues: 1-1132 <NAK>
12	139.0	2.3	1.460	1	EDBE1P	A; Cross-references: UNIPROT:O14746; EMBL:AF015950; NID:92330016; PIDN: AAC51672.1; PID:9
13	139.5	2.3	0.552	2	F75311	A; Experimental source: kidney
14	138.5	2.3	0.924	2	S27923	C; GenBank accession: AF015950
15	135	2.3	1.356	2	C45219	A; Gene: TRT
16	134.5	2.3	0.946	2	JC7810	A; Map position: 5p
17	133	2.2	0.606	2	G75302	B; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
18	133	2.2	1.106	2	J00405	C; Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
19	132	2.2	0.860	2	S55543	D; Query 1 MPRAPCRAVRSILRSHYREVLPLATEFVRLGPQCMWLRGDDVYLHLLARCALFVLPSCAYOVCGPPLYQLGA 60
20	131.5	2.2	1.184	2	G01763	E; Db 1 MPRAPCRAVRSILRSHYREVLPLATEFVRLGPQCMWLRGDDVYLHLLARCALFVLPSCAYOVCGPPLYQLGA 60
21	131	2.2	1.446	1	A45344	F; Db 1 MPRAPCRAVRSILRSHYREVLPLATEFVRLGPQCMWLRGDDVYLHLLARCALFVLPSCAYOVCGPPLYQLGA 60
22	130.5	2.2	1.184	2	S50832	G; Db 1 DARRPPAAPEFQVSCLEKELVARYLQRLCERGANVNLAFGLDARGGPPEAFTTSVR 120
23	130.5	2.2	2.715	2	T13049	H; Db 1 DARRPPAAPEFQVSCLEKELVARYLQRLCERGANVNLAFGLDARGGPPEAFTTSVR 120
24	129.5	2.2	0.383	2	S32975	I; Db 1 SYLPNTVTDALRGSGAWGLLRLRGGDYLHLLARCALFVLPSCAYOVCGPPLYQLGA 180
25	129	2.2	4.03	2	S52796	J; Db 1 SYLPNTVTDALRGSGAWGLLRLRGGDYLHLLARCALFVLPSCAYOVCGPPLYQLGA 180
26	129	2.2	1.776	2	G86280	K; Db 1 ATQARPPPHASGPRLGGERANHHSVREAGVPLGLPAPGARRGGSASRSLPLPKRPRR 240
27	128.5	2.2	0.628	2	S01955	L; Db 1 ATQARPPPHASGPRLGGERANHHSVREAGVPLGLPAPGARRGGSASRSLPLPKRPRR 240
28	128	2.1	0.376	2	C75580	M; Db 1 GAAPBEPERTVQGSGWAHPTRGSGDRGFCVVSPARPAEATLEGALSQTRISHPSVG 300
29	127.5	2.1	1.048	2	T31425	N; Db 1 GAAPBEPERTVQGSGWAHPTRGSGDRGFCVVSPARPAEATLEGALSQTRISHPSVG 300



QY	971 RRKLFGVLRKXCHSLFLDLQVNSLQTVCTNLYKILLQAYRFHACVULQLPFHQQWIK-NP	1029	Db	201 RTIETSIQNSKARK-----EVSW-----	219
Db	965 RQKLCYFLVPCPCHPLFDNSNIGELVRLNLYQITFLAANKFHCYVYEV---SREWKLHP	1021	Qy	286 EGALLGTRHS---HPGVGROHAGPIPSTSRPRPNDTPCPVYAYETRKHF-LYSSGDKREQLR	342
Qy	1030 TFLFLRVTISDTASLCSYSLKAKNAGMSLAGKA-GAAAGPLSEAVQMLQHAQFLKLTRHRT	1089	Db	220 -NSISISRSRPFYRSYKK-----FKDQLYNUHSICDRTNVT	256
Db	1022 QTLFRKPTISYTRMFLINRVRRTNGSSFRVPLKLYKEBEVIVLGLDAYIQVULKKKNSR	1081	Qy	343 PSFLLSSLRPSLTG-----ARRLVETIFLGSRPMMPGTPRRL---PRLPQRYWMQRPL	392
Qy	1089 YVPLIGSLRTAQTO---LSRKLPGTLTALBAAANDL	1123	Db	257 -MMWQWIPQRQFGILNAFOVQKQHVKVPLBQTAKLHLR	312
Db	1082 YRMLLIYTLKSLAHSLSQQLSSELYATDRSNSSSL	1118	Qy	393 FLELIGNHACQPYGYLLKTHCPLRAATPAAGVACAREKPGSVAAPEEEDTDPRRLVQLL	452
<b>RESULT 3</b>					
T03838	telomerase catalytic chain - fission yeast (Schizosaccharomyces pombe)		Db	313 SLSKVNH-YCPY---IDTH-----DDE-----KIL	334
N;Alternate names: telomerase reverse transcriptase_1			Qy	453 RQHSSWQYQGTVRACLRLVPPGLWSRHNERRFLRPLRNTYKFKISIGKHAKLISQEBETWKM	512
C;Species: Schizosaccharomyces pombe			Db	335 SYSLRPNQVPAFLRSILVRFPKLIGNQRLIFEFLKLSRYESFSLHYLMSNI	394
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004			Qy	513 SVRDCAWL---RRSPCGVCPAAEHLRREELTAKPLHLWMSVYVYLRSFFYVTTETTFQ	569
C;Accession: T03838; T03339; T40085			Db	395 KISIEIWLVLGKRSRNSKMCU---SDPEBKQJFAFEFLWYLYNSFIPILQSFYITBSSDL	452
R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.			Qy	570 KQFLRPFYRKSVWSKLSQISIGIRQLHKLKVQLRLELSAEVRQHREARPALTSRLFLPKPDG	629
Science 277, 955-959, 1997			Db	453 RNRRTYFRKDWW-KLICRPPITTSKMEAFKINENNRVMDTQ-KTLLPPAVTRLPLPKNT	510
A;Title: Telomerase catalytic subunit homologs from fission yeast and human.			Qy	630 LRPIYNMDYVVGARTERREKAAEFLTSRVALSFVLYNEPARP-----GLLGASVGL	683
A;Reference number: Z15111; MUID:97400623; PMID:3252327			Db	511 FRLTNTL-----RKRFLIKQNGNSKMLVST-----NOTLRPVASILKHLINEESSGI	558
A;Accession: T03838			Qy	684 D---DTHRAWRTF---VLRVTAQDPPPELKFVQDVTGATDTPDRLTEVTASITKPN	737
A;Status: preliminary; translated from GB/EMBL/DBJ			Db	559 PPNLEYVMKULTEKDLKHERMFG---RCKYFVRLDIKSCYDRIKQMLFRIVKKLKDPE	616
A;Molecule type: DNA			Qy	738 TYCVRYYAVVQKAIGHVKAFKSHVSTLTLQPYPMRQFYAHLLQETSPRLDAVIEQSSS	797
A;Residues: 1-989 <NAK>			Db	617 -FVIRKYATIHK-ATSDRATKQFVSEAFSVDMPPEKFVQVLLSMKTS---DTLFYDFVDY	671
A;Cross-references: UNIPROT:O13339; EMBL:AF015783; PIDN:92340167; PIDN:AC49803.1; PID:92			Qy	798 LNEAASSGLFDVFLRPMCHHAIRGKSYVOCQGIIQGSISLSTLSCYGDMEKLPGI	857
A;Experimental source: strain 972h(-)			Db	672 WTKSSSEIFMLKELSGHIVKGNISQYLOKVGIIQGSISLSSFLCHFYMEDLIDBEYLTSFT	731
A;Accession: T03839			Qy	858 RRDG-LLRLRYDFFLUTPHLTAKTFLTRVTPYEEVNLKTVNFPVEDEBALGG	916
A;Status: preliminary; translated from GB/EMBL/DBJ			Db	732 RKKGSVSLRQVDDFLITVANKDAKFLNLSLRGERHNFTSLEXTVINFENSGIINN	791
A;Molecule type: DNA			Qy	917 TAFVQMPAHGLFPWCGLLDTRLEV---QSDYSSYARTSIRASLTENRFGKAGRNM	971
A;Residues: 1-524, 526-989 <NA2>			Db	792 TFFENBSKCR--MFFGFSVNMRSIDTLACPKIDALFNTSVLTKHMGKSF-----	842
A;Cross-references: EMBL:AF015783; PIDN:92340167; PIDN:AC49802.1; PID:92340168			Qy	972 RKLFGVYLRKHS---LFLDQVNSLQTVCTNLYKI-----LLDAY	1010
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.			Db	843 -FYKILRSSLASFAQVFDITHNSKPNSCCNITRGYSMCMRAQAY	887
Submitted to the EMBL Data Library, March 1998					
A;Reference number: Z21904					
A;Accession: T40085					
A;Status: preliminary; translated from GB/EMBL/DBJ					
A;Molecule type: DNA					
A;Residues: 1-524, 526-989 <LYN>					
A;Cross-references: EMBL:AL022299; PIDN:CAA18391.1; GSPDB:GN00067; SPDB:SPBC29A3.14C					
A;Experimental source: strain 972h-; cosmid c29A3					
C;Genetics: trt1; SPBC29A3.14c					
A;Map position: 2					
A;Introns: 86/3; 113/3; 153/2; 241/1; 372/1; 395/3; 485/3; 524/3; 582/2; 644/1; 693/3; 7					
C;Keywords: alternative splicing					
Query Match	10.0%	Score 594.5; DB 2; Length 989;			
Best Local Similarity	22.3%	Best Local Similarity 22.3%; pred. No. 2.e-32;			
Matches 238; Conservative 202; Mismatches 380; Indels 247; Gaps 42;					
5 PRCRAVSLLSLRSHYREVPLATEVRIGPQGMWLVYORGDDAFAFLVAQCL-----	55				
Qy	7 PKSRILR-FLENQYVYLCTLNDYV-----QLVLRGSPASSYNSNCECERLSRDSYQTSFS	57			
Db	56 -----YCPWDARPPDAPSPRQVSCSCK-ELIVARYLQLRCERG---AKVNTAFLGPAL-LD	105			
Qy	58 IFLHSTVGFDSKPDGEV-QFSSPKCSQSELIANVYKQMFDESFERRNLIMKGFMSMNH	116			
Db	106 GARGGPPPEAFTTSVRYLPTNTVDAIRGSGWAGWLRLARCAFLVWAPS	165			
Db	117 DERAMHNGVQNDLVSFPTNVLISLSE-SKWLQLLIEIGSDAMYLSSGSIFALPND	175			
Qy	166 CAYQVCPPLQYOLGAATQARPPPHASGRRRLGCEBAWNTSVREAGVPLGLPAPGARRG	225			
Db	176 NYLQIISGCIPLPK-----SKRKR	200			
Qy	226 GSASRSIPLPKRPRGAAPEPRTVGQGSWAHPGRTGSPSDRGFCVSPARPAEATSL	285			

RESULT 4  
T31107 telomerase reverse transcriptase - Oxytricha trifallax  
C;Species: Oxytricha trifallax  
C;Accession: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: T31107  
R;Bryan, T.M.; Speerger, J.M.; Chapman, K.B.; Cech, T.R.  
Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998  
A;Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytricha  
A;Reference number: Z20985; PMID:98337940; PMID:9671703  
A;Accession: T31107  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1132 <BR>  
A;Cross-references: UNIPROT:076332; EMBL:AF060230; PIDN:93342795; PIDN:AA  
C;Genetics: TERT  
A;Gene: TERT

Query Match	6.6%; Score 395; DB 2; Length 1132;	Qy	322 PFWYAAETKHFLLYSGSGDKEQILRPSFTLSSLRPSLTCGARRVETIIFLGSRWWMPGPRLER 381.
Best Local Similarity	22.2%; Pred. No. 1e-18;	Db	239 PGFV-KSSEPNYS----EIKKGQFKVQKLGQRO----FINSDKIKPDPQTQIK 286
Matches	136; Conservative 114; Mismatches 305; Indels 58; Gaps 15;	Qy	382 --LPQRY----WQMRPFILE--LIGNHACQPYGVLLKTCPLRAAVTPAGVCA 428
Qy	450 QLRLRQSSPQVYGFVRACLRLYPPGLWSRHNERFLRNTKFKFISLGKHAKLSQLBLT 509	Db	287 KTLKBEYQSKNFSCQEDRFLFLEETEKVQNPHINENVLLKCKL----333
Db	451 QLFYEQQDQBOISNPLTEFVANVPEPKNFDEGK-NKKTPKNNQKQFVKNPESFTKISLL 509	Qy	323 PFWQYQGFVRLQHRS----SPWQYQGFVRLQHRS----
Qy	510 WICMSYRDCAWIIRRSPVGCVPAAFH--PLREELAKELIHLMSVYVTELLRSFTYET 566	Db	239 PGFV-KSSEPNYS----EIKKGQFKVQKLGQRO----FINSDKIKPDPQTQIK 286
Db	510 NKFRYNEVSLN----SFKCDENKFKFMNENEVFFKVLKWKYFEDLIAITLARCYFSTEK 565	Qy	382 --LPQRY----WQMRPFILE--LIGNHACQPYGVLLKTCPLRAAVTPAGVCA 428
Qy	567 TFOKNRLLFFYRKSYWSKSYKLOSIGTRQHLLKRVQRLSEAEVROREARPALITSRQFPIK 626	Db	287 KTLKBEYQSKNFSCQEDRFLFLEETEKVQNPHINENVLLKCKL----333
Db	566 AKEYORIIFYRKSYKRNWNMMRLSDDLLKQ-NIKQVEKEMRFLCESQ-NFADGKDRKLIP 623	Qy	429 EKPOGSVAAPBEETDPRRLUVLQRQHS----
Qy	624 PDGLRPIVNMDDVYVGARTPRRE----KRAERLTSRKV--ALFSTVNTYERARRPGLLG 677	Db	334 -----PENYQSLKSQVKQIYQSENKANOQSCENLFLSYDTEISYKQTINFLRQI 384
Db	624 GDTFRPIM-----TENRKTPNQVGKFEQSRMTMINKLQTAHMMKNUKSKMFKHSFG 674	Qy	470 RRLVPGGLGSRHERRFRFLRNTKFKFISLGKHAKLSQLPLTWKMSVRDCAWLRSPGVGCY 529
Qy	678 ASVGLDDIHLRAWTFVLRVRAODPPLPELYFKVDTGAYDTIIPQDRLTENIAS----731	Db	385 QNCVPNQNLGKK-NFKVFLKLEKLYEFVQMKRPNENQVLY1CFMDVDFEWF----V 435
Db	675 FAYPNYDILMKRKENFVOKWK-QINSPALFYAMDIKCYDNDCERVNNFLQKSQDLMDK 733	Qy	530 PAAEHLR----REBILAKFLHNLMSVYVYELLRSFFYETTFQKNRBLFYRKSV 580
Qy	732 -----LIKPTONTCYVRAYVQKAHGHVRKAFKSHVSTLTDLQPYMRQFV AHLQET 783	Db	436 DLKQKFTOKRKYISDKRKLGDLLIVFINKLKVIPVILYNTKEKEGSQFYVRKPI 495
Db	734 EYFLNLTFLVLRKNNIVLVERSNSFRKLPIKQYERYKFK-IGIDGSSYPTLFEILLEDEFND 792	Qy	581 W----SKUQSIGI-RQHLLKRVOLRELSAEVRQHREARPALLTSRLRIPKPDGLRPVNM 636
Qy	784 SPLRDAYVVEIQSSSLNBAASSGLFDFVFLRPMCHAVAIRGKSYVQOCGIPQGOSLSTLCC 843	Db	496 WKLVSKLTVKLEENLKEVEKLIPEDSFQKYPQ----GKURIPKIGSFRPIM- 546
Db	793 LANKKRTTIVEQEORKKFKPKNDLQPVNLKICQNNYTFENKQYKQKMGKIPQGLCYSYILSS 852	Qy	637 DYVVGARTFRREKRAERLTSRKVAKLFS----VLYNVEFARRPGLGASVGLGDDIHRAWT 692
Qy	844 JCYGDMENKMLKFLGAFIRRD-----GULLRIVDDPFLVTPHLTHAKTFLRLTVRGVPEX 894	Db	547 -----TFLRKDKQKVNKLNLNQNLMSQVFLRNQKNDLQKQISEKFAQ 599
Db	853 FYYANLLEENALQFLRKSMMDPEKPEINLMLTDDYLLMTTEKNNMLFTEKLQLSLN 912	Qy	583 GYRKAFKSHVSTLTDLQ----PYM----RQFV AHLQE----782
Qy	895 GCVVNLLRKTVNPFVEBALGTTAFYQ--MPAHGLFPWCGLLDIDTRTLEQVDSSYAR 951	Db	659 PLIQQQTNNNSAMEEKEEINKKPKFMNDINFPYFNLERQLAYSLYDDDDQILQKG 718
Db	913 FFCKFMKCLKTKNFAFLNQKIGCNTNTQDIDSINDFLHWGKISDITKUNIQI-NRK 971	Qy	783 -----TSPLRDAYVVEIQSSSLNEASSGLFDFVFLRPMCHAVIRGKSYVQOCGIPQGOSLIS 838
Qy	952 TSTRASLTFENRGFKAGNMRRLKLFGVLRLKCHSLFLDQVNSLQTVCTNQYKILLQAYR 1011	Db	719 FKEIQSDDRPFTIVNQDKPRCITKODIHNHLKHSISQYNTFSNKVFKRQKGIPQGLNIS 778
Db	972 EGILCTIANNQNTNESTLWLKKLKSFLMANNISFYFKSTINTKOFANTILSKUYAAEK 1031	Qy	839 TLLCSLCYGDMDENKMLKFLGAFIRRD----GILLRLYDDEFLLVTPHLTHAKTFLRLTVRGV 891
Qy	1012 PHACVQLCP-PHQ 1023	Db	779 GYLCSFYGKLEEEVTFQFLKNAEQYNGSTINLMRLTDYLFISDSQQNALNLIVQLQNC 838
Db	1032 YVACQCFKRFHE 1044	Qy	892 PEYGCUVNLKTVVN--FPEDEAUGTAFVQMPAHGLFPWCGLLDTRTLEQVDSSY 949
Qy	14891 telomerase (EC 2.7.7.7) catalytic chain p133 - Tetrahymena thermophila	Db	839 NNGNEFNDQITTFNQFQDYNL--EHFKISVNECOWIGKSIDMNTLEIK--SIQ 892
N;Alternate names: telomerase reverse transcriptase		Qy	950 ARTSIAASLTENRGFKAGNMRRLKFGVLRKCHSLFLDQ----QVNSLQTVCTNQY 1002
C;Species: Tetrahymena thermophila		Db	893 KQTQBEINQNTINVAISI-KHLLSKQKKNLR----SLFNUQLDIFYNPNTNSFEGICRQIX 947
C;Accession: T14891		Qy	1003 --KILLOQAYRFHACVQLQL----PHEHQVWK--NPTFFLRVISDTAS---LCY- 1044
R;Collins, K.; Gandhi, L.		Db	948 HHSKATVMKVFYPMFTKLQFIDLKRSKQSYQGKENTNFNLKQLYTVEDVCKILCYL 1007
Proc. Natl. Acad. Sci. U.S.A. 95, 8485-8490, 1998		Qy	1045 -----SILKAKAGMISLGAKGAGAPLSEAVQWLCHIA 1077
A;Title: The reverse transcriptase component of the Tetrahymena telomerase ribonuclease		Db	1008 QFEDIEINSNKEIPRNLYSWIMDIDIVSYLKKQQ----FKGSYLNKLK----- 1050
A;Reference number: 218252; MUID: 98337941; PMID: 9671704		Qy	1078 FLLKLTTRHRYTVYPL-LGSLRATQQLSRKLPGTTLTALEAAANPALPSDFKTL 1131
A;Status: preliminary; translated from GB/EMBL/DBJ		Db	1051 -LQKIRKSRSEPFYLGEGCKSLQLLISQQVQNLNKELEIEFDLNLNIQDICTL 1104
A;Molecule type: mRNA			
A;Residues: 1-111 <COL>			
A;Cross-references: UNIPROT:077448; EMBL:AF061284; PID:93335167; PRID: AAC3			
A;Gene: TERT			
C;Genetics: SGCS			
C;Keywords: nucleotidyltransferase			

RESULT 6

S53336 telomerase catalytic chain EST2 - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein L84312; protein YLR318w

C;Species: Saccharomyces cerevisiae

C;Date: 05-May-1995 #Sequence\_revision 01-Sep-1995

C;Accession: S53396



Db	2970	AVAAVAAAQAEGVRRREGPPVVRARSADHGEDALLALPPY-TMLEFAQKYFRDPQRQQ 3028	Qy	298	SVGRQHAGGPSTSRPPRPM-DTPCPP-----VIAETKHLYSSGDKE-----QLR 342
Qy	782	E-----TSPIDAVVIEQSSLLNEAASSGLEDVFRMCHAVR 819	Db	421	PPGAGQRPSSOPTGGRPAAGAPGTPAAGPGGGAAVPGSGATPHERGSGPADPAAALLP 480
Db	3029	DGLALKSRPRESSTLEDMLCFTXTPLQESLISLSSLSKWDATMDMLAVNRFMGDAPLK 3088	Qy	343	PSFLIUSLRLPSLTLARRLVETIFFGSRPMPG----TPLLRLPQ-----RYPQM 389
Qy	820	IRGKSYVQCGIPQGSIISLTLSCLGD--MENKAFAGI-----RRDG 861	Db	481	PERQEPRLFQDAAQRCP----AGPPPTTRSGAAQQRTHRPPGCRSPARNPCCPRTWR 536
Db	3089	GQSDIDVLCN-----LKLKC-GDHEVNRDECYCOVVKQITNTSSKQDSCQRGW 3136	Qy	390	RPLFLLELLGNNHAQCPTYGVLLKTHCPL--RAAVTPAAGYCAREKPGQSYAAPESEDTDPR 447
Qy	862	LLRLUVDFE---LLVTPHLTHAKTFRTLVR--GVPBYG----CYNVLRKTVNNPVED 911	Db	537	RS----GAQRGHPFPGAGQRSPGPTGGRPAAPGAPGTPAAPGGGAAPSGATPHPER 591
Db	3137	RLLQXVATAYHSCSEVLPHLTR--FLQDVSRTPGFLFQGIAKACEQNLQKTL-----3186			
Qy	912	EAUJGTAFYQMPAHGLFWCGLILJLDTTRLEVSDYSSYARATSIASLTLTENGFKAAGRMR 971			RESULT 9
Db	3187	-RFGG-----RLFLPSS-----IELRAML-----AGRSSK 3210			AS935
Qy	972	RKLFLF---GV-----LRLKCHSLFLDQLQNLQTVCT-----NIYKILLQAYRFA 1014			unconventional myosin-15 - mouse
Db	3211	RQLFLPPGLERHLKIKTCVADL-----VEEICAMALATPPEAFNEYVIFVUTNTRGGHV 3266			C;Species: Mus musculus (house mouse)
Qy	1015	CVL-----QLPFPHQWKNPTEF-----LRLVSDTASLCY 1044			C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
Db	3267	CPLSRAYILDVASEMROQDGSSYMLMRRVLWDQPLKFNENLYTVMHYNOVLPDYLKGLF 3326			C;Accession: A59255
Qy	1045	SLIKRKNAGMGSIAKGAGLPEAFCYQWLCHOAFLKLTKTHRVT--YVPLLGTSURTAQ- 1100			A;Status: preliminary; not compared with conceptual translation
Db	3327	SSVSPASR-----PSEQ--LHQQVSKLASLORAKDHFTYLP---SVREYQE 3366			A;Molecule type: mRNA
Qy	1101	---TOLSRKLPGTT 1111			A;Cross-references: UNIPROT:Q9QZZ4; GB:AF144095; PID:96224684; PID:AAF05904.1; PID:962
Db	3367	YIPAQLLRTTAGST 3380			C;Genetics:
					A;Gene: MGI:Myo15
					A;Cross-references: MGI:1261811
					A;Map Position: 11:33.9
					F:1209-1871/Domain: myosin motor domain homology <MMO>
					Query Match 2.4%; Score 144; DB 2; Length 3511;
					Best Local Similarity 17.6%; Pred. No. 0.68; Gaps 44;
					Matches 189; Conservative 117; Mismatches 385; Indels 380;
					Query 3 RAPRCCRARSLLRSHYREVPLATFVRLFGQWRVLRQGSDPAAFRALVQCLVCVP---59
					Db 677 RPPRLASPYGSIQRQH-----PPW-----APAPAHFPPQQA 707
					60 -WDARPPAA-----PSFQVQSCUKELYARVLQBLCEGAKNVLAEGFA 102
					708 NWGFAEPPGTSPEVADLLAFTPVRPSFR-----ASRSRSRRAAYGFP 751
					103 LDGAGGCPPEAFTSVRSVLPTNTD-ALRGSSAWGLLRLRVDVLYHLLARCALFV 160
					752 -----SPSLIGRRRSPQSPQSLSPQGQ-----778
					161 LVAPSCAYQVCGPPLYQLGQATQAPPAPHASGPRLGERAANNVISREAGVPLG-----215
					Db 779 -----YHSPGIGLSPQLSRLRGFPQPPFPQPPRQPOSUREAF-SLRASGRJGPPRSP 830
					216 -----LPAGARRRGGSASRSLPLPKR-----PRRGAAPEPRT-----PVGQGS 255
					Query Match 2.9%; Score 172.5; DB 1; Length 660;
					Best Local Similarity 26.1%; Pred. No. 0.00078; Gaps 16;
					Matches 94; Conservative 16; Mismatches 159; Indels 91; Gaps 16;
Qy	167	AYQVG--GPPLYQLGAATAQAA-RPPPHASGPRRRLGCRRAWNHSVREAGVPLGLPAPGAR 222	Db	831 VLGSSPRPSPPPLKGHRPSLNPSPSLPRTWRLSEPTPRAVPPWHRAYPPPSAQP 890	
Db	244	AAQRCPAGPPPTGAAATRTHRPPGCRSAANPGCRTRW-----RSGAQORGHPPGAG 300	Qy	256 WAHPGTRGRPSDRCGFCVYSPARAEATSLLEGALGSTRSHSHPSVGRHHAGPPSTSRRPR 315	
Qy	223	RQGSSAASLSP-LPKRPRGAAPEP-ERTPVQGSMWHPGRFRGSPDRFCV-VSPAR-- 277	Db	891 W---EASTGAL-----QENOREAESETSEPTVPPPLAPSMDVDMPTQRPBS 935	
Db	301	QRPSPGTPGRPAAGPCTPAAGPQGGGAAPGSPATPHPERGSGPADPAAARLPPQE 360	Qy	316 PWDTPC-----PPVIAETKHLFLYSS-----GDKEQRLRPSFLS 348	
Qy	278	-----PAAEATSLLEGAL-----SGTRHSHP 297	Db	936 PWPEGIGSLRGFSRPPVPPENPLLETSPOSEDRVSNLTGFQQLHHDDGPQLTK 995	
Db	361	PRLPQDILAAAQRCRCPAGPPTRSSAAAQTHRRPPGCPRTWRRSGAORGHP 420	Qy	349 SLRPLGTLARRVETFLGSRSPWMPGTPRPL-PRLFORYWOMRPLFLFLGNH-----400	
					996 SADESFL--EKPEEEVNTLGD-PQPAEPEBALNTPNKNVVSERKVLRSAS-PLVTCOK 1051
					401 --AQCP-----YGVLLKTHCPLRAAVTPAAGYCAREKPGQS-----434

Db	1052	ARATWPOWHRWKTVSRTPAAPLAPTRAPGPIKAGECOPRAEGRFPAVMQVRGSSSFREK	1111	Db	1473	PGSRPGGGSYSHP-----HPPQSPSLSPHSJPPHPSYPPDPPSPHTPHSPPLPTSPHGP	1525
Qy	435	---VAAPBEEDTDPRR-----LVLQLURQHSSPWQYGFVDRAC	468	Qy	332	LYSSGSDKEQLRSPFILLSLRPSLTCARRLVTIFLGSRPW	371
Db	1112	GPAPVOPPQPPDQPEQGPQAQCSLRWMLWPPTDANLWSRRTYSSQSHLRGHGDC	1171	Db	1528	LHASCPQAQTPPP--VQTPPSQA-----GSAPW	1554
Qy	469	LLRL---VPPGLNGSRHNRERLRTKKEFSLGRKHAKLSLTWMKMSYRCAWLRRSPG	525	RESULT 11			
Db	1172	HKSLSWKCTRPQSW---QNKHSIRNLPSMRSRBREDEVDMTQLEIDQETTVLAN	--1225	T18314	hypothetical protein L7610.4 - Leishmania major		
Qy	526	VGCYPAAEHLBREELTAKU-----WMLMSVYVYVLLRSP-----FVYT	564	C;Species: Leishmania major			
Db	1226	-----LXTRFERMLIYTGSTLVSVNPNYRMFAIYGPQQVQOYSGRALGENPPBHLFAIA	1279	C;Accession: T18314	#sequence_revision 15-Oct-1999	#text_change 09-Jul-2004	
Qy	565	ETTFQK-----NBLFFYR-----KSVSKL-----QSGTIROHHLKRVOLRESE	603	R;Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Rajandream, M.; Iyer			
Db	1280	NLAFAKMLDAKQNCVIISSGESGSGKTEAKLIRCLAMNQQRDVMQKIKLEATPLIE	1339	submitted to the EMBL Data Library, May 1999			
Qy	604	A-----EVROHREARPAALLTSRRLRFKPDGLRPIVNMDDYVVGARTFRREKRAE-----	653	A;Reference number: Z18876			
Db	1340	AFGNAKTVNDNSSR---FGKFVIEFLEGVICBAAITSQYLLEKSRIVFQAKNERNYH	1396	A;Accession: T18314			
Qy	654	-----LTSRKVAKLFSVLYE-----RARPGGLGASVGLDIDHRWTFVLRVRAQD	701	A;Status: preliminary; translated from GB/EMBL/DBJ			
Db	1397	YELLAGLPLQQLRQAFSLSQLEQATYYLNQGNCLEAGKS---DADDFRR-----	1441	A;Molecule type: DNA			
Qy	702	PPPLPFYKVWDVGTAYDTIPQDLTEVIAI-----IKEQNTYCVRRAVVQKAAGHVRKAFKS	761	A;Residues: 1-1892 <OLI>			
Db	1442	-----LLAMEVLG-FTSQQDTSFRLSILHGNVYPERKHEHDAQFAY-----	1485	A;Cross-references: UNIPROT:097007; EMBL:AL034356; PID:e1371878; NID:e1371559; PID:e1371559; P			
Qy	762	HVSTLTDQPYMQRQFHQLQETSP---LRDAVIVBQOSSSLNEASSGGLFDFVLFRMCHHAVR	819	C;Genetics:			
Db	1486	SWVSAREIAQ-----VAEILQVSBEGLQKAITFVKTETIRE-----KIFTPLTVESAVD	1534	A;Note: L7610.4			
Qy	820	IRGKSYVQCGIPQGSILSTLICSLCYGMDMENKLFGI-----PRDCUILLVLID	868				
Db	1535	AR-----DATAKVLVALLFGMLITRNLAVLSPKQDTLSTIAILD	1572				
RESULT 10							
T00090							
		hypothetical protein KIAA0522 - human (Fragment)					
C;Species: Homo sapiens (man)							
C;Accession: T00090							
R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.							
DNA Res. 5, 31-39, 1998							
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complete							
A;Reference number: Z14086; MUID:98290545; PMID:9628581							
A;Accession: 00000							
A;Status: preliminary; translated from GB/EMBL/DBJ							
A;Molecule type: mRNA							
A;Residues: 1-1560 <NR>							
A;Cross-references: UNIPROT:O60275; EMBL:AB011094; NID:g3043557; PID:BA25448.1; PID:g3							
A;Experimental source: brain; Clone: HG1393							
A;Genetics:							
A;Note: KIAA0522							
Query Match							
Best Local Similarity	2.4%	Score 142.5; DB 2;	Length 1560;				
Matches	65;	Conservative 15; Mismatches 89;	Indels 51; Gaps 12;	RESULT 12			
				EDB1IF			
Qy	173	PPLQLGAAATQARPPPHASGPERRRLGCERAWHNSVREACVP-----LGLPAPGARRGG	226	immediate-early protein IE180 - simid herpesvirus 1 (strain Indiana-Funkhauser)			
Db	1365	PPLQLGQSL-----PPPSAP-----FVGPHR-----HFAHARGVPGPHYHTGPRGPAPRAG	1415	C;Species: simid herpesvirus 1			
Qy	227	SASRSPLPLPKRP-----RGAAPPERPVGCGWSWAHFGRTGPSSDRGFCVSPARAEATSL	285	C;Accession: S04713	#sequence_revision 30-Jun-1990	#text_change 09-Jul-2004	
Db	1416	GHPQFAPHRPLHQLOPTSPPLSPAPQHPAH-----KQCPKHF1PSHHPQMMPAAGAGG	1472	R;Cheung, A.K.			
Qy	286	EGAL-----SGTRHSHPSVGROHAGPSTSR-----PPRPWDTPCPCPVYAETHF-----	331	Nucleic Acids Res. 17, 4637-4646, 1989			
				A;Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies virus			
				A;Reference number: S04713; MUID:89313207; PMID:2546124			
				A;Molecule type: DNA			
				A;Accession: S04713			



Qy 338 KEQLRPSFLSLRPSLTLGARRLVEVIFLGSRPWMPG-TPR-RL-PRLPORYWQMRPLFL 394  
 Db 182 EPTTR--LQPATPRSGAAADPDPGHPAAAPRPEPEPRTRLQPATPRSGAAADP--A 235

Qy 395 ELLGNH1QCPYGVLLKTHCPLRAAVTAAAGVYCAREKEQGSVAAPEEEEDTPRRLVQ 450  
 Db 236 DPVG-HPAAPRPGPBPTRLQPATPRSGAAADPVGHPAAAPRPGPBPTRLQ 290

RESULT 15

C45219  
 N-methyl-D-aspartate receptor chain NMDAR2D-1 - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: C45219  
 P;Ishii, T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadonani, H.; Yokoi, M.; Akazawa  
 J. Biol. Chem. 268, 2836-2843, 1993  
 A;Title: Molecular characterization of the family of the N-methyl-D-aspartate receptor  
 A;Reference number: A45219; MJD:93155102; PMID:8428958  
 A;Accession: C45219  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-1156 <ISH>  
 A;Extraneous source: brain  
 A;Note: sequence extracted from NCBI backbone (NCBIP:124264)  
 C;Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology  
 F;451-879/Domain: glutamate receptor homology <GRH>

Query Match 2.3%; Score 135; DB 1; Length 1356;  
 Best Local Similarity 27.2%; Pred. No. 0.76; Gaps 22;  
 Matches 88; Conservative 16; Mismatches 102; Indels 118; Gaps 22;

Qy 59 PWDARPPAA----PSFRQVSCLKEVAVLQRLCERGAKNVLAGPALLDG----- 106  
 Db 1084 PRRAAPPVCAVLDLPS-----PSDSESDSESLGGASIGGLEPWWFA 1124

Qy 107 -----ARGGPPEAFTTSVRSYLPNTVTDAIRG--SGANGILLRRVGGDDVLVHLJARCA 157  
 Db 1125 DFPYPYAZERLGPGRWWSV-----DKUGWRAGSWSWYLPPIKPGP--AWHCRHCA 1172

Qy 158 LFVLPAP----SCAYQWC----GPPYQLGAATQARPPHASGP---RRRLGGERAWN 204  
 Db 1173 SLELLPPPRHLSCHDGLGGMWAPP-----PPWAAGPPPRERARCGCPRPHP 1221

Qy 205 HSVREA-GVPLGLPAPARR--GG-----SASSL-PLPKRPRGAAPPEET-PVG 252  
 Db 1222 HRPRASHRPAAPAHHRHRAAGGWDFPPPAPESTSELDISRP---CP-PHRTGDTG 1276

Qy 253 QGSWAHFGRTTQPSDRFCVYSP-----ARPAEEATSLEGALSGTRHSHPSVRQHHA 305  
 Db 1277 AGTWAHAGALR-----ISPAWSRVDADAPPTPAAPSVSA---GGPGRGAKWT 1324

Qy 306 GPPSTSR----PPR--FWDTPCPP 323  
 Db 1325 GPSWVGDRNGFGRTPGAAASCAP 1348

Search completed: January 10, 2005, 17:39:30  
 Job time : 57 secs

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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:19:31 ; Search time 168 Seconds (without alignments)

2417.152 Million cell updates/sec

Title: US-10-053-758-225

Perfect score: 5961

Sequence: 1 MPRAPCRRAVRSILRSHYRE.....TALEAAANPALPSDFKTLID 1132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A\_Geneseq\_23Sep04 : \*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

RESULT 1  
AAW46957

ID AAW46957 standard; protein; 1132 AA.

XX AAW46957;

AC XX

DT 13-AUG-1998 (first entry)

DE Human telomerase reverse transcriptase.

XX Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; N-termina

XX cell proliferation; cancer; ageing; ribonucleoprotein.

XX Homo sapiens.

OS Homo sapiens.

XX PN 62317891-A.

XX PD 08-APR-1998.

XX PP 01-OCT-1997; 97GB-00020890.

## SUMMARIES

\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## DESCRIPTION

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	1132	2 AAW46957	AAw46957 Human tel
2	5961	100.0	1132	2 AAW90251	AAw90251 Human cat
3	5961	100.0	1132	2 AAY28881	Aay28881 Human tel
4	5961	100.0	1132	2 AAY32050	Aay32050 Human tel
5	5961	100.0	1132	2 AAY43621	Aay43621 A human t
6	5961	100.0	1132	2 AAY26580	Aay26580 Human tel
7	5961	100.0	1132	2 AAG64859	Aag64859 Heart mus
8	5961	100.0	1132	4 AAG64329	Aag64329 Human pro
9	5961	100.0	1132	4 AAB9930	Aab9930 Human tel
10	5961	100.0	1132	4 AAB82765	Aab82765 Human tel
11	5961	100.0	1132	5 AAE29226	Aae29226 Human tel
12	5961	100.0	1132	5 AAU72735	Aau72735 Human tel
13	5961	100.0	1132	6 ABR42364	Abr42364 Human tel
14	5961	100.0	1132	6 ABR2053	Abr2053 Human tel
15	5961	100.0	1132	6 ABP56676	Abp56676 Human tel
16	5961	100.0	1132	6 ABR58045	Abr58045 Human tel
17	5961	100.0	1132	7 ADD21420	Add21420 Human TER
18	5961	100.0	1132	7 ADR72743	Adr72743 Human pro
19	5961	100.0	1132	8 ADG70114	Adg70114 hTERT pro
20	5961	100.0	1132	8 ADG9059	Adg9059 Human TER
21	5961	100.0	1132	8 ADI82172	Adi82172 Human tel
22	5961	100.0	1154	2 AAW61350	Aaw61350 Human tel
23	5961	100.0	1189	2 AAW47008	Aaw47008 Glutathio
24	5955	99.9	1285	2 AAW47000	Aaw47000 HIS tagge
25	5954	99.9	1132	2 AAW71376	Aaw71376 Human tel

The present sequence represents human telomerase reverse transcriptase (hTRT), which is a ribonucleoprotein. The present invention also describes the following methods: (A) determining whether a test compound

CC



nucleic acids inhibit telomerase action (by binding to specific mRNA), particularly in neoplastic cells and may be expressed in vivo. Antibodies and fragments of the protein, used as probes or primers, are used to diagnose telomerase-related conditions (especially neoplasia) by (i) detecting abnormal levels of the subunit protein in body fluids or tissues or (ii) by measuring the amount of the encoding nucleic acid. Expression of the nucleic acid encoding the subunit mRNA is confined to tumour cells, in contrast to the ubiquitous expression of the telomerase

Sequence 1132 AA:	Q	Query Match Score 5961; DB 2; Length 1132;	Db	841 ICSLCYGDMENTKLFGAGRTRDGGLLRLRVDLFLVTPHLTHAKTFLRTLVGPEYGCVNLL 900
Best Local Similarity 100.0%; Pred. No. 0;	Qy	901 RKTIVNFPVEDALGGTAFVQMPAHGLFPWCGLLDIDTRILEQSDYSSARTSRAASLTIF 960		
Matches 1132; Conservative 0; Mismatches 0; Gaps 0;	Db	901 RKTIVNFPVEDALGGTAFVQMPAHGLFPWCGLLDIDTRILEQSDYSSARTSRAASLTIF 960		
Y	Y	1 MPRAPRCAVRSLSRSHYREVLPLATEVRIGPQWRLVORGDAFAFRALVAQCLVCVPW 60		
b	b	1 MPRAPRCAVRSLSRSHYREVLPLATEVRIGPQWRLVORGDAFAFRALVAQCLVCVPW 60		
Y	Y	61 DARPPAAPSFRQVSCLKELEVRLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVR 120		
o	o	61 DARPPAAPSFRQVSCLKELEVRLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVR 120		
Y	Y	121 SYLPNTVTDALRGSGAWGLLIRRGGDVLVLLARCAFLVAPSCAYQVCGPPLYQLGA 180		
o	o	121 SYLPNTVTDALRGSGAWGLLIRRGGDVLVLLARCAFLVAPSCAYQVCGPPLYQLGA 180		
Y	Y	181 ATOARPPPHASGPERRRLGCERAWHNSVREACVPLGLPAPGARRGGSASRSLPLPKRPR 240		
o	o	181 ATQARPPPHASGPERRRLGCERAWHNSVREACVPLGLPAPGARRGGSASRSLPLPKRPR 240		
Y	Y	241 GAAPPERTVQGGSWAHPGTRGSDRGFCVWSPARPABATSLSLEGALSTRHSHPSVG 300		
o	o	241 GAAPPERTVQGGSWAHPGTRGSDRGFCVWSPARPABATSLSLEGALSTRHSHPSVG 300		
Y	Y	301 RQHHAGPPSTSRRPPREWDTCPVYAAETKHFLYSSSDKEQRLRPSFLSSRPSLTCARRL 360		
o	o	301 RQHHAGPPSTSRRPPREWDTCPVYAAETKHFLYSSSDKEQRLRPSFLSSRPSLTCARRL 360		
Y	Y	361 VETIPLGSRWPMPGTPRRLPLPQLPORYWQMPRLFLEIIGNHAQCPYCVLKKLTHCPLRAAVT 420		
o	o	361 VETIPLGSRWPMPGTPRRLPLPQLPORYWQMPRLFLEIIGNHAQCPYCVLKKLTHCPLRAAVT 420		
Y	Y	421 PAAGYCAREKPGQSYAAPEEEDTDPRLVQQLRHOSSPMQVYGFYRACRLRVLUPPGIWS 480		
b	b	421 PAAGYCAREKPGQSYAAPEEEDTDPRLVQQLRHOSSPMQVYGFYRACRLRVLUPPGIWS 480		
Y	Y	481 RHNERFLRNTKKFISLGKAHLSQLBLTWNMSVRDCAWLRLSPGTYGCVPAAEHRLREEI 540		
b	b	481 RHNERFLRNTKKFISLGKAHLSQLBLTWNMSVRDCAWLRLSPGTYGCVPAAEHRLREEI 540		
Y	Y	541 LAKETHLWMLMSVYVYELLRSFYYVTTETFOKNRLFFYRKSYWSKLSQIGIRHLKRLQRLS 600		
o	o	541 LAKETHLWMLMSVYVYELLRSFYYVTTETFOKNRLFFYRKSYWSKLSQIGIRHLKRLQRLS 600		
Y	Y	601 LSEAEVROHREARPALTSRLRFLPKDGLRPTVMDYVCAFRERERERLTSRVA 660		
b	b	601 LSEAEVROHREARPALTSRLRFLPKDGLRPTVMDYVCAFRERERLTSRVA 660		
Y	Y	661 LFSVLYNERARRPGLGASTGLDDIHRARTFVLVRAODDPPELYFVQVDTGAYDTI 720		
o	o	661 LFSVLYNERARRPGLGASTGLDDIHRARTFVLVRAODDPPELYFVQVDTGAYDTI 720		
Y	Y	721 PQDRTEVIAISIKPONTYCVRYAVYQKAAGHGVKAFKPSHVSHTLTDQPYMROYAH 780		
b	b	721 PQDRTEVIAISIKPONTYCVRYAVQKAAGHGVKAFKPSHVSHTLTDQPYMROYAH 780		
Y	Y	781 QETSPRLDAYVIEQSSSLNEASSGLDPEVFRMCHAVRIGKSYVQCGIPQGSILSTL 840		
o	o	781 QETSPRLDAYVIEQSSSLNEASSGLDPEVFRMCHAVRIGKSYVQCGIPQGSILSTL 840		
Y	Y	781 QETSPRLDAYVIEQSSSLNEASSGLDPEVFRMCHAVRIGKSYVQCGIPQGSILSTL 840		
Y	Y	841 LSCLCYGDMENTKLFGAGRTRDGGLLRLRVDLFLVTPHLTHAKTFLRTLVGPEYGCVNLL 900		

CC	therapeutic agents, for inhibition of telomerase expression and activity		
SQ	Sequence 1132 AA;		
Query Match	100.0%; Score 5361; DB 2; Length 1132;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 1132; Conservative 0; Mismatches 0; Gaps 0;			
QY	1 MPRAPCRAYRSLLSHREVLPLATFVRRLGPQGWRLVQRGDPAFAFLVALVAOCLVCPW 60		
DB	1 MPRAPCRAYRSLLSHREVLPLATFVRRLGPQGWRLVQRGDPAFAFLVALVAOCLVCPW 60		
QY	61 DARPPPAAPSFROYSCLEKELVARYLQLRCERGAKVLARGFALLDGAAGGPPAAFTTSYR 120		RESULT 4
DB	61 DARPPPAAPSFROYSCLEKELVARYLQLRCERGAKVLARGFALLDGAAGGPPAAFTTSYR 120		AAY32090 standard; protein: 1132 AA.
QY	121 SYLPLNTVDALRGSAWGLLRLRRYGDVVLHLLARCAFLVLPASCAYQVCGPPLYQJGA 180		AAY32090 ID; AAY32090 standard; protein: 1132 AA.
DB	121 SYLPLNTVDALRGSAWGLLRLRRYGDVVLHLLARCAFLVLPASCAYQVCGPPLYQJGA 180		XX
QY	181 ATQARPPPHASGPERRRLGCBRANNHSVREAGVPLGLPAGARRGGSASRSLPLPKRPR 240		XX
DB	181 ATQARPPPHASGPERRRLGCBRANNHSVREAGVPLGLPAGARRGGSASRSLPLPKRPR 240		DT 17-JAN-2000 (first entry)
QY	241 GAAPEPRTVPGCGSWAHPGRTRGFSDRGFCVCWSPARABEATLLEGALSGTGHSHPSVG 300		XX
DB	241 GAAPEPRTVPGCGSWAHPGRTRGFSDRGFCVCWSPARABEATLLEGALSGTGHSHPSVG 300		DE Human telomerase reverse transcriptase (hTRT).
QY	301 ROHHAGPPTTSRPRPWPDTCPCPYYAETKHFYLISSGDKBQLRSPFLLSLRPSLTGARL 360		XX
DB	301 ROHHAGPPTTSRPRPWPDTCPCPYYAETKHFYLISSGDKBQLRSPFLLSLRPSLTGARL 360		XX
QY	361 VETIFLGSRREWMPGTPTPLRPLPORYWQMPRPLFELLGNAHQCPYGVILKTHCPLRAVT 420		XX
DB	361 VETIFLGSRREWMPGTPTPLRPLPORYWQMPRPLFELLGNAHQCPYGVILKTHCPLRAVT 420		XX
QY	421 PAAGVCAREKPKGSVAAPPEEFTDPRRLVQLLROHSSPQVQYGVFRACLRRLVPPGIGWS 480		XX
DB	421 PAAGVCAREKPKGSVAAPPEEFTDPRRLVQLLROHSSPQVQYGVFRACLRRLVPPGIGWS 480		XX
QY	481 RHNERFLNNTKEFISLGKAHLSLQELTWKMSYRDCAWLRRSPGVCYPAAEHRLREI 540		XX
DB	481 RHNERFLNNTKEFISLGKAHLSLQELTWKMSYRDCAWLRRSPGVCYPAAEHRLREI 540		XX
QY	541 LAKFDHWAISVYVYELLRSPPYTTFTQKRLFPRKSVWSLQOSIGTRQHILKRVQRE 600		XX
DB	541 LAKFDHWAISVYVYELLRSPPYTTFTQKRLFPRKSVWSLQOSIGTRQHILKRVQRE 600		XX
QY	601 LSEAEVROHREARPALLTSRLREPKPDKHARPTYNNMDYVGARTFRERKAERLTSYKA 660		XX
DB	601 LSEAEVROHREARPALLTSRLREPKPDKHARPTYNNMDYVGARTFRERKAERLTSYKA 660		XX
QY	661 LFSVNLNEYERRARRPGHLGASVYGLDDIHARWTFYVLRQDPPELYFKVDTGAYTTI 720		XX
DB	661 LFSVNLNEYERRARRPGHLGASVYGLDDIHARWTFYVLRQDPPELYFKVDTGAYTTI 720		XX
QY	721 PQDRITEVASIIKPNQNTCYVRRYAVQXAAHGVKAKSHVSTLTDIQLPYMRQFYV AHL 780		XX
DB	721 PQDRITEVASIIKPNQNTCYVRRYAVQXAAHGVKAKSHVSTLTDIQLPYMRQFYV AHL 780		XX
QY	781 QETSPRLDAVVIQESSLINEAASSGLFDYFLRFMCHHAVRIGKSYVOCOGIPQGSLTSTL 840		XX
DB	781 QETSPRLDAVVIQESSLINEAASSGLFDYFLRFMCHHAVRIGKSYVOCOGIPQGSLTSTL 840		XX
QY	841 LCSLCYGMENKLPAFAGIRDGLLRLVDDFLYVPHLTHAKTFPLTLYGVPYGCVN 900		XX
DB	841 LCSLCYGMENKLPAFAGIRDGLLRLVDDFLYVPHLTHAKTFPLTLYGVPYGCVN 900		XX
QY	901 RKTIVNPFVPEDEALGGTAVQMPAHGLFPMCGLLDQVYDSSYARTSIRASITP 960		XX
DB	901 RKTIVNPFVPEDEALGGTAVQMPAHGLFPMCGLLDQVYDSSYARTSIRASITP 960		XX
QY	961 NRGPXAGNMRRKLFGVLRKCHSFLFLDQVNLSQTVCCTNIKILLQDAYRPHACVQLP 1020		XX

1	MPRAPRCAVRLSRSYREVPLATVRLQCLVCPW	60	Db	1081 KLTRHRVTVVPLLSLRTAQTLSRKLPCTTLTAAANPALPSDFKTLID	1132
61	DARPPAPSPFQVSCKRELARVLQCLCERAKNVLAFGFAIDLGARGPPBAAFTSVR	120		RESULT 5	
61	DARPPAPSPFQVSCKRELARVLQCLCERAKNVLAFGFAIDLGARGPPBAAFTSVR	120		AAV43621	
121	SYLPNTVTDALRGSGAWGLLRLRVGDPLVHLLARCLFVLVAPSCKYQVCGPPLYOLGA	180		ID AAV43621 standard; protein: 1132 AA.	
121	SYLPNTVTDALRGSGAWGLLRLRVGDPLVHLLARCLFVLVAPSCKYQVCGPPLYOLGA	180		XX	
181	ATQARPYPHASPRRIGCERAWHNSREAGVPLGLDAPGARRGGASRSPLPKPDR	240		AC AAV43621;	
181	ATQARPYPHASPRRIGCERAWHNSREAGVPLGLDAPGARRGGASRSPLPKPDR	240		XX	
241	GAAPERPRTPVQGGSWHPGTRGPSPRGFCVSPAPAEATSLSLEGALSCTRHSHSSVG	300		DT 26-JAN-2000 (first entry)	
241	GAAPERPRTPVQGGSWHPGTRGPSPRGFCVSPAPAEATSLSLEGALSCTRHSHSSVG	300		XX	
301	RQHHAGSPSTSRRPSPDTPCPVYATPKFLYSSGKDEOLRSPSLTSLRPLGARRL	360		DB A human telomerase reverse transcriptase (TRT) polypeptide.	
301	RQHHAGSPSTSRRPSPDTPCPVYATPKFLYSSGKDEOLRSPSLTSLRPLGARRL	360		XX	
361	VETIFLGSRPMPMGTDRPLPRLPQTYWQMRPFLLELGNHAQCPYGLLTKTCPLRAVT	420		KW Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;	
361	VETIFLGSRPMPMGTDRPLPRLPQTYWQMRPFLLELGNHAQCPYGLLTKTCPLRAVT	420		KW dendritic cell; telomerase activity; cancer cell; proliferating cell;	
421	PAAGYCAREKPGQSYAEEPEEDDPFLVLQJLQRQHSPSPWQYQFVRLCLRLVPPGWLGS	480		KW immunological; destruction; telomerase; cancer; proliferation disease.	
421	PAAGYCAREKPGQSYAEEPEEDDPFLVLQJLQRQHSPSPWQYQFVRLCLRLVPPGWLGS	480		XX	
481	RHNERRFLRNTKKFISIGKHAKLSQLPLTWKMSVRCawlRSPGCVPAAEHRLRBEI	540		OS Homo sapiens.	
481	RHNERRFLRNTKKFISIGKHAKLSQLPLTWKMSVRCawlRSPGCVPAAEHRLRBEI	540		XX	
541	LAKFLEWLMSTVVLLRSFFVTTETFQDRQLEFFKTSWISKLQSGLRQLKRVLRE	600		XX	
541	LAKFLEWLMSTVVLLRSFFVTTETFQDRQLEFFKTSWISKLQSGLRQLKRVLRE	600		XX	
601	LSEAETYRQHREARPALIITSRLRPIKEDGLRPTVNMDDYVGARTFREKRAERLTSRKVA	660		XX	
601	LSEAETYRQHREARPALIITSRLRPIKEDGLRPTVNMDDYVGARTFREKRAERLTSRKVA	660		CC The present sequence represents a human telomerase reverse transcriptase (TRT) polypeptide. The protein is used in the method of the invention.	
661	LFSVINYERARRPGLGASVGLDDIHRWTAQDPPPELYFKVYDVTGAYDTI	720		CC The specification describes a method for activating a T cell, that	
661	LFSVINYERARRPGLGASVGLDDIHRWTAQDPPPELYFKVYDVTGAYDTI	720		CC comprising contacting the T lymphocyte with a dendritic cell that	
721	PQDRLETVIASIKPONTYCVRAYVQKAAGHVRKAFKSHVSTLTDLQPMRQFV AHL	780		CC expresses a TRT peptide in the context of a MHC CLASS I or MHC CLASS II molecule.	
721	PQDRLETVIASIKPONTYCVRAYVQKAAGHVRKAFKSHVSTLTDLQPMRQFV AHL	780		CC The protein causes induction of an in vivo immunological	
781	QETSPILRDVTEQSSLNEASGLFLFVLFRMCHIAVRIGKSYQCGQFPGSITLSTL	840		CC response to telomerase activity. Cancer cells are characterized by	
781	QETSPILRDVTEQSSLNEASGLFLFVLFRMCHIAVRIGKSYQCGQFPGSITLSTL	840		CC expression of endogenous TRT gene and the presence of detectable	
841	LCSLCYGDMEKILFAGIRRDGILRLVYDDELLVTPPHLTHATPLFLRIVGPEYGCVNL	900		CC telomerase activity. Therefore, by eliciting a specific immune response	
841	LCSLCYGDMEKILFAGIRRDGILRLVYDDELLVTPPHLTHATPLFLRIVGPEYGCVNL	900		CC to TRT or to TRT-expressing cells, it is possible to selectively target	
901	RKTVVNPFPVEDALGGTAFVMPAHGIFPWCCLLDTPLTEYQSDYSYARTSIRASLTF	960		CC proliferating cells for immunological destruction. The method is used for	
901	RKTVVNPFPVEDALGGTAFVMPAHGIFPWCCLLDTPLTEYQSDYSYARTSIRASLTF	960		CC eliciting an in vivo immune response to telomerase by activating a T	
961	NRGFKAGRNMERKLFGYTLRKLCHSLSLFLQYNSLQTYKILLQAYRFHACVQLQP	1020		CC lymphocyte, and is useful for prevention and treatment of cancers and	
961	NRGFKAGRNMERKLFGYTLRKLCHSLSLFLQYNSLQTYKILLQAYRFHACVQLQP	1020		CC other proliferation diseases/conditions	
7	Sequence 1132 AA;			XX	
841	DARPPAAPSFRQVSCLKEVLVARNLQRLCERAKNVLAFGLDARGGPPBAAFTSVR	1		Query Match 100.0%; Score 5961; DB 2; Length 1132;	
841	DARPPAAPSFRQVSCLKEVLVARNLQRLCERAKNVLAFGLDARGGPPBAAFTSVR	1		Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps	
901	SYLPNTVTDALRGSGAWGLLRLVYDDELLVTPPHLTHATPLFLRIVGPEYGCVNL	960		Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps	
901	SYLPNTVTDALRGSGAWGLLRLVYDDELLVTPPHLTHATPLFLRIVGPEYGCVNL	960		1 MPRAPRCAVRSLLRSYHREVPLATEFVRLGPQGWRVLRGDPAAFLVQCLVCPW	6
961	SYLPNTVTDALRGSGAWGLLRLVYDDELLVTPPHLTHATPLFLRIVGPEYGCVNL	960		1 MPRAPRCAVRSLLRSYHREVPLATEFVRLGPQGWRVLRGDPAAFLVQCLVCPW	6
961	SYLPNTVTDALRGSGAWGLLRLVYDDELLVTPPHLTHATPLFLRIVGPEYGCVNL	960		61 DARPPAAPSFRQVSCLKEVLVARNLQRLCERAKNVLAFGLDARGGPPBAAFTSVR	1
961	SYLPNTVTDALRGSGAWGLLRLVYDDELLVTPPHLTHATPLFLRIVGPEYGCVNL	960		61 DARPPAAPSFRQVSCLKEVLVARNLQRLCERAKNVLAFGLDARGGPPBAAFTSVR	1
1021	PHQYWKNPFTFLRIVSDTASLCSYSLKAKNAGMSLGAKGAGPLPSEAOWLCHQPL	1080		121 SYLPNTVTDALRGSGAWGLLRLVYDDELLVTPPHLTHATPLFLRIVGPEYGCVNL	1
1021	PHQYWKNPFTFLRIVSDTASLCSYSLKAKNAGMSLGAKGAGPLPSEAOWLCHQPL	1080		121 SYLPNTVTDALRGSGAWGLLRLVYDDELLVTPPHLTHATPLFLRIVGPEYGCVNL	1
1081	KLTRHRVTVVPLLSLRTAQTLSRKLPCTTLTAAANPALPSDFKTLID	1132		181 ATQARPYPHASPRRIGCERAWHNSREAGVPLGLDAPGARRGGSSAASP1L1PKPDRR	1

Db	181	ATQARPPHASGRRRJUCERAWNHSYREAGYPLGLPAGARRGGSASRSLPLPKPRRR	240	KW	Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
Qy	241	GAPEPERTPVGQSGWAHPGRTRPSDGFCTVSPPARAEATSLEGALSGTRPHSPVG	300	KW	immunogen; enzyme; telomerase-mediated DNA replication; human.
Db	241	GAPEPERTPVGQSGWAHPGRTRPSDGFCTVSPPARAEATSLEGALSGTRPHSPVG	300	KX	Homo sapiens.
Qy	301	ROHHAGPSTSRRPRTDPCPVAETKHFYSSGDEQRLRPSFLSLRPSLTGARRL	360	KX	W0927113-A1.
Db	301	ROHHAGPSTSRRPRTDPCPVAETKHFYSSGDEQRLRPSFLSLRPSLTGARRL	360	PD	03 - JUN - 1999.
Qy	361	VETIFLCSRPMNGTPRPLRQYQWQMRPLFELIGHNAACPYGULLKTHCPLRAAVT	420	KX	98WO-US025211.
Db	361	VETIFLCSRPMNGTPRPLRQYQWQMRPLFELIGHNAACPYGULLKTHCPLRAAVT	420	XX	25 - NOV - 1998;
Qy	421	PAAGVCAKEPKQGSVAAPEEEDTPRVLVQLRQHSSPQVYGFVRACLRLVPPGLWGS	480	XX	97US-00979742.
Db	421	PAAGVCAKEPKQGSVAAPEEEDTPRVLVQLRQHSSPQVYGFVRACLRLVPPGLWGS	480	XX	98US-00042460.
Qy	481	REINERRFLRNTKFKFISLGKHAKLSQLQETLWMSVRDCAWLRLSPGCVPAAEHRLREI	540	XX	(GERO-) GERON CORP.
Db	481	REINERRFLRNTKFKFISLGKHAKLSQLQETLWMSVRDCAWLRLSPGCVPAAEHRLREI	540	XX	(YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
Qy	541	LAKELHLMSTVYELLRSFPEYVETTEFQKRNLFYTKRSVWSKLSQGIRQLKRYQLE	600	XX	PA Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
Db	541	LAKELHLMSTVYELLRSFPEYVETTEFQKRNLFYTKRSVWSKLSQGIRQLKRYQLE	600	XX	PT nucleic acids.
Qy	601	LSBAEVQRQHREARPALLTSRURFLPKEDGLRPIKEDGLRPIKEDGLRPIKEDGLR	660	XX	XX Disclosure; Fig 3; 135pp; English.
Db	601	LSBAEVQRQHREARPALLTSRURFLPKEDGLRPIKEDGLRPIKEDGLRPIKEDGLR	660	XX	CC The invention relates to a mouse telomerase reverse transcriptase (mTERT) enzyme. Compositions containing mTERT can be used in telomere length assays. Isolated mTERT is useful as an immunogen for the production of monoclonal or polyclonal antibodies. The method is useful for assessing the degree of purification and identification of new mTERT species, such as an mTERT allele, homolog or isoform, or to screen for modulators (antagonists and agonists) of telomerase-mediated DNA replication.
Qy	661	LFSVLYNTERARRPGLIGASVLGLDDTHRAWRFLVRAQDPPPELYFKVYDVTGAYDTI	720	XX	CC Antagonists and agonists of mTERT can be used to modify the activity of other telomerase enzymes such as human TERT (hTERT). The present sequence represents a human TERT enzyme
Db	661	LFSVLYNTERARRPGLIGASVLGLDDTHRAWRFLVRAQDPPPELYFKVYDVTGAYDTI	720	XX	CC
Qy	721	PDRLTEVIASIKPQNTYCVRYAVQKAAIGHVTKAFKPSVSTLTDLQPMRQV AHL	780	XX	CC
Db	721	PDRLTEVIASIKPQNTYCVRYAVQKAAIGHVTKAFKPSVSTLTDLQPMRQV AHL	780	XX	CC
Qy	781	QETSPRDVAVTQEQQSSLINEASSGLFDYFLRMCHHAIRGKSYVQCGIFQGSILSTL	840	XX	CC
Db	781	QETSPRDVAVTQEQQSSLINEASSGLFDYFLRMCHHAIRGKSYVQCGIFQGSILSTL	840	XX	CC
Qy	841	LCSLCYGDMEENKLFLAGTRDGLLRLYDDEFLVTPHLTHAKFLFLRTVRYGPEYGCVN L	900	QY	1 MPPAPRCAVRSILRSHYREVPLATFVRLLGPGQWRLVQRGDPAAFRALVAQCLVCPW
Db	841	LCSLCYGDMEENKLFLAGTRDGLLRLYDDEFLVTPHLTHAKFLFLRTVRYGPEYGCVN L	900	Db	1 MPPAPRCAVRSILRSHYREVPLATFVRLLGPGQWRLVQRGDPAAFRALVAQCLVCPW
Qy	901	RKTVDVNPVEDALGGTAFVQMPAHGLFWMCILLDTTLEQSDISSYARTSIRASLT F	960	QY	61 DARPPPAAPSFROVSCILKELVARVLQRLCERGAKNVLAFGFLAIDGARGGPPEAFTTSYR
Db	901	RKTVDVNPVEDALGGTAFVQMPAHGLFWMCILLDTTLEQSDISSYARTSIRASLT F	960	Db	61 DARPPPAAPSFROVSCILKELVARVLQRLCERGAKNVLAFGFLAIDGARGGPPEAFTTSYR
Qy	961	NRGFKAAGRNMRRKLFGVYLRKCHSLFLDQVNSLQTYCTNLYKILLQAYRFHACVQLQP	1020	QY	121 SYLINTVTDALGSGAGCILLLRQGDDVYVHLARCALFVULVSCAVQVCGPPLYOLGA
Db	961	NRGFKAAGRNMRRKLFGVYLRKCHSLFLDQVNSLQTYCTNLYKILLQAYRFHACVQLQP	1020	Db	121 SYLINTVTDALGSGAGCILLLRQGDDVYVHLARCALFVULVSCAVQVCGPPLYOLGA
Qy	1021	FHQQWKNPFTFLRVLISDTASLCYSLIKAKNAGMSLGAKGAAGPLDSEAVQWLCHOAFL L	1080	QY	181 ATQARPPPHASGRRLGGERAWHNSYREAGYPLGLPAGARRGGSASRSLPLPKPRR
Db	1021	FHQQWKNPFTFLRVLISDTASLCYSLIKAKNAGMSLGAKGAAGPLDSEAVQWLCHOAFL L	1080	Db	181 ATQARPPPHASGRRLGGERAWHNSYREAGYPLGLPAGARRGGSASRSLPLPKPRR
Qy	1081	KLTRHRVTVYVPLGSLRATQTLTALAAANPALSDFKTLID 1132	1132	QY	241 GAAPEPRTPVGCGSWAHGPRTRGSDRGFCVVSPPARAEATSLLEGALSGTRHSHPSVG
Db	1081	KLTRHRVTVYVPLGSLRATQTLTALAAANPALSDFKTLID 1132	1132	Db	241 GAAPEPRTPVGCGSWAHGPRTRGSDRGFCVVSPPARAEATSLLEGALSGTRHSHPSVG
Qy	301	AAAY26580 standard; protein; 1132 AA.	301	QHHAAGPSTSRRPRTDPCPVYAYETKHFYLYSGDKEQLRPSFLSSLRPLSLTGARRL	361
Db	301	AAAY26580	301	RQHHAAGPSTSRRPRTDPCPVYAYETKHFYLYSGDKEQLRPSFLSSLRPLSLTGARRL	361
Qy	361	VETIFLCSRPMNGTPRPLPQRYWQMRPLFELIGHNAACPYGVLLKTHCPLRAAVT	424	XX	424
Db	361	VETIFLCSRPMNGTPRPLPQRYWQMRPLFELIGHNAACPYGVLLKTHCPLRAAVT	424	XX	424
Qy	421	PAAGVCAKEPKQGSVAAPEEEDTPRVLVQLRQHSSPQVYGFVRACLRLVPPGLWGS	480	XX	480

Db	421	PAAGVCREREKPGSVAAPEEEDTPRRLVQLLROHSSPWQYGFTRACRLRVLPPGLWGS	480	XX	Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
Qy	481	RHNERERFLRNTKKFISLGKHAKLSQLBLTWSMVRDCAWIIRRSPGVCYPAAEHRLREB1	540	PI	Yamada Y;
Db	481	RHNERERFLRNTKKFISLGKHAKLSQLBLTWSMVRDCAWIIRRSPGVCYPAAEHRLREB1	540	XX	WPI ; 2001-42556/45.
Qy	541	LAKELHMLMSTYVVELLRSFFYVTTETFQKNRLFFYKRSWNSKLOSSIGIRQLKRVQLE	600	DR	N-PSDB ; AAH48235.
Db	541	LAKELHMLMSTYVVELLRSFFYVTTETFQKNRLFFYKRSWNSKLOSSIGIRQLKRVQLE	600	XX	Cells capable of differentiating into cardiomyocytes and originating in bone marrow or umbilical blood cells for study of cardiomyocyte differentiation and treatment of heart disease.
Qy	601	LSEAEVTRQHREARPALTSRLFIPKPGDRPIVNMDDYVGARTPRREKAERLTSRVKA	660	PT	PT
Db	601	LSEAEVTRQHREARPALTSRLFIPKPGDRPIVNMDDYVGARTPRREKAERLTSRVKA	660	XX	XX
Qy	661	LFSVNLXERARRPGLIGASVIGLDDIHRANTFVLRVRAODPPELYFVKVDVTGAYDT1	720	PS	PS
Db	661	LFSVNLXERARRPGLIGASVIGLDDIHRANTFVLRVRAODPPELYFVKVDVTGAYDT1	720	XX	Claim 87; Page 143-147; 183pp; Japanese.
Qy	721	PQDRLTVIASIPIKPOINTCYCVRAYAVYQKAAGHGVKAFKSHVSTLTDIQPYMRQFVAHL	780	CC	The present invention provides cells originating in the human bone marrow or umbilical blood cells which are capable of differentiating into cardiomyocytes. These cells are useful in the treatment of diseases involving heart muscle degeneration, such as myocardial infarction, and the study of cardiomyocyte differentiation. The present sequence is a protein described in the exemplification of the invention
Db	721	PQDRLTVIASIPIKPOINTCYCVRAYAVYQKAAGHGVKAFKSHVSTLTDIQPYMRQFVAHL	780	CC	CC
Qy	781	QETSPRLDAVIEQSSSLNEASSGLPFDVFRMCHAVLRGKSVYQCGQIPQSSILSTL	840	CC	CC
Db	781	QETSPRLDAVIEQSSSLNEASSGLPFDVFRMCHAVLRGKSVYQCGQIPQSSILSTL	840	XX	XX
Qy	841	LCSLCYGDMEKLFLAGTRDGLLFLVDFLFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL	900	SQ	Sequence 1132 AA;
Db	841	LCSLCYGDMEKLFLAGTRDGLLFLVDFLFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL	900	DB	Query Match 100.0%; Score 5961; DB 4; Length 1132;
Qy	901	RKTVVNFPIVEDBALGTTAFYQMPAHGFLFPMCGLLDTRTLEQVSDYSYARTSIRASLTF	960	DB	Best Local Similarity 100.0%; Pred. No. 0;
Db	901	RKTVVNFPIVEDBALGTTAFYQMPAHGFLFPMCGLLDTRTLEQVSDYSYARTSIRASLTF	960	Qy	Matches 1132; Conservative 0; N mismatches 0; Indels 0; Gaps 0;
Qy	961	NRGFKAGRMRKLFQVLRKCHSLFLDLQVNSLQTCINIKILLQAYRFHACVLQLP	1020	DB	1 MPRAPCRAVRSLSRSHREVLPLATEVRLGPQSWRLVQRGDPAFRALVAQCLVCPW 60
Db	961	NRGFKAGRMRKLFQVLRKCHSLFLDLQVNSLQTCINIKILLQAYRFHACVLQLP	1020	Qy	1 MPRAPCRAVRSLSRSHREVLPLATEVRLGPQSWRLVQRGDPAFRALVAQCLVCPW 60
Qy	1021	FHQQWKNPTEFLRVTISDTASLCYSLTKAKNAGMGLGKAAQGPISPEAVQWLCQAFEL1	1080	DB	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
Db	1021	FHQQWKNPTEFLRVTISDTASLCYSLTKAKNAGMGLGKAAQGPISPEAVQWLCQAFEL1	1080	Qy	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
Qy	1081	KLTRHRTVYYPLGLSIRTAQTLRSRKLPGTTLTALEAANPALPSDEKTYLD	1132	DB	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
Db	1081	KLTRHRTVYYPLGLSIRTAQTLRSRKLPGTTLTALEAANPALPSDEKTYLD	1132	Qy	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
RESULT 7				DB	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
ID	AAG64859	standard; protein; 1132 AA.		Qy	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
XX	AAG64859;			DB	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
XX	21-SEB-2001	(first entry)		Qy	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
XX	DE	Heart muscle cell differentiation related protein SEQ ID NO: 31.		DB	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
XX	DE	Heart muscle cell; human; cell differentiation; heart disease.		Qy	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
XX	OS	Homo sapiens.		DB	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
XX	PN	WO200148151-A1.		Qy	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
XX	PD	05-JUL-2001.		DB	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
XX	PF	27-DEC-2000; 2000WO-JP009323.		Qy	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
XX	PR	28-DEC-1999; 99JP-00372826.		DB	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
XX	PR	28-FEB-2000; 2000WO-JP001148.		Qy	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
XX	PR	02-NOV-2000; 2000WO-JP007741.		DB	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL
PA	(KYOW )	KYOWA HAKKO KOGYO KK.		Qy	61 DARPPPAAPFQYQSCILKEVARYLQRUCERGAKNVLAFCALPFLVTPHILTHATKFLTRLVRGKSVYQCGQIPQSSILSTL

Query Match 100.0%; Score 5961; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCAVRSLRSHREVLPLATFVRLGPQWRLVQRGDPAAFRLVAQCLVCPW 60

Db 1 MPRAPRCAVRSLRSHREVLPLATFVRLGPQWRLVQRGDPAAFRLVAQCLVCPW 60

Qy 61 DARPPAAPSFRQSCILKELVARVLRQLCERGAKNVIAFGFALLDGARGGPPPEAFTTSVR 120

Db 61 DARPPAAPSFRQSCILKELVARVLRQLCERGAKNVIAFGFALLDGARGGPPPEAFTTSVR 120

Qy 121 SYLNTNTDALRSQGAWGILLRQGDDVYLHARCALFVLVAPSCAYQVCGPLLYQGA 180

Db 121 SYLNTNTDALRSQGAWGILLRQGDDVYLHARCALFVLVAPSCAYQVCGPLLYQGA 180

Qy 181 ATQRPPHASGRRRLGCERAMHNSYREAGVPLGLPAGRGGSASRSLPLPKPRRR 240

Db 181 ATQRPPHASGRRRLGCERAMHNSYREAGVPLGLPAGRGGSASRSLPLPKPRRR 240

Qy 241 GAAPEPERTPVGGGSWAHPGRTRGSPDRGFCVSPARPAEATSLLEGALSGTRHSHPSVG 300

Db 241 GAAPEPERTPVGGGSWAHPGRTRGSPDRGFCVSPARPAEATSLLEGALSGTRHSHPSVG 300

Qy 301 RQHAGPSTSRRPRPNDTPCPVYAAETKHFYSSCDKEOLRSPFLSSLRPSLTGARRL 360

Db 301 RQHAGPSTSRRPRPNDTPCPVYAAETKHFYSSCDKEOLRSPFLSSLRPSLTGARRL 360

Qy 361 VETIFLGSRPNMPTPRLPRLPRLPQRYWMQMPFLLELGNHQCPGVLLKTHCPRLRAVT 420

Db 361 VETIFLGSRPNMPTPRLPRLPRLPQRYWMQMPFLLELGNHQCPGVLLKTHCPRLRAVT 420

Qy 421 PAGVCAKRECPQGSSAYPEEEEDTPRLVQLRQHNSSPWQVQYGFVACRLRLVPPGLWGS 480

Db 421 PAGVCAKRECPQGSSAYPEEEEDTPRLVQLRQHNSSPWQVQYGFVACRLRLVPPGLWGS 480

Qy 481 RHNERFLRNTKKFISLGKHAKLSQLBLTQVDSVRCAWLJRSRGVGYCPAAEHHLREEI 540

Db 481 RHNERFLRNTKKFISLGKHAKLSQLBLTQVDSVRCAWLJRSRGVGYCPAAEHHLREEI 540

Qy 541 LAKFLHMLMSYYVVELRSFFYVTTETFOKNRLPYFKRSWSKLSQIGIROLHKVQLRE 600

Db 541 LAKFLHMLMSYYVVELRSFFYVTTETFOKNRLPYFKRSWSKLSQIGIROLHKVQLRE 600

Qy 601 LSEAEVQHREARPAALTSURFPIPKDGRPIVNDYVVGARTFREKERAERLTSRVKA 660

Db 601 LSEAEVQHREARPAALTSURFPIPKDGRPIVNDYVVGARTFREKERAERLTSRVKA 660

Qy 661 LFSV1AYERARRPGLGASVILGLODIIHRAWRTEFLVRRAODPPPELYFVKVDVTGAYDTI 720

Db 661 LFSV1AYERARRPGLGASVILGLODIIHRAWRTEFLVRRAODPPPELYFVKVDVTGAYDTI 720

Qy 721 PQDRLTIVIASIKPONTYCVRVYAVOKAAGHGYRKAFKSHVSTLTDLQPYMRQFVAHL 780

Db 721 PQDRLTIVIASIKPONTYCVRVYAVOKAAGHGYRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy 781 QETSPRLDVTAVVIEQSSSLNEASGGEDPVLFRMCHAVRJRGKSYVQCGIPOGSILSTL 840

Db 781 QETSPRLDVTAVVIEQSSSLNEASGGEDPVLFRMCHAVRJRGKSYVQCGIPOGSILSTL 840

Qy 841 LCSLCYGDMDENKLPGIRRQGLLFLVDDFLVTPHLTHATKFLRLVRGVPEGCCVNL 900

Db 841 LCSLCYGDMDENKLPGIRRQGLLFLVDDFLVTPHLTHATKFLRLVRGVPEGCCVNL 900

Qy 901 RKTVNFPVDEALGSTAQVMPAHGLFPWCGLJLIDTRTLEQVQSSYARTSIRASLT 960

Db 901 RKTVNFPVDEALGSTAQVMPAHGLFPWCGLJLIDTRTLEQVQSSYARTSIRASLT 960

Qy 961 NRGFAGRNNMRKLCFGLKCHSFLDQVNSLQCTVCPNNIKYKILLQAYRFHACVLQJP 1020

Db 961 NRGFAGRNNMRKLCFGLKCHSFLDQVNSLQCTVCPNNIKYKILLQAYRFHACVLQJP 1020

Sequence 1132 AA;

XX

AC

XX

DT 24 -SEP-2001 (first entry)

XX

DE Human protein #2.

XX Angiogenesis; cardiant; cell differentiating agent; bone marrow; heart muscle cell; heart disease; human.

XX OS Homo sapiens.

XX PN WO200148149-A1.

XX PR 28-DEC-1999; 99JJP-00372826.

XX PD 05-JUL-2001.

XX PF 28-FEB-2000; 2000WO-JP001148.

XX DR WPI; 2001-418452/44.

DR N-PSDB; AAH49601.

XX New adult bone marrow-originated cells capable of differentiating into heart muscle cells, applicable as remedies for various heart diseases particularly with damaged heart muscle accompanying degeneration.

XX Disclosure; Page 128-134; 158pp; Japanese.

XX The present invention relates to cells isolated from bone marrow, which are capable of at least differentiating into heart muscle cells. The cells are applicable as remedies for various heart diseases particularly with damaged heart muscle accompanying degeneration. The present sequence was used to illustrate the present invention.

XX Sequence 1132 AA;

QY 1021 FHQQWQKNPFFLRVISDTASLCYSILKAKNAGMSIAGKGAAGPLPSEAYOWLCHOAFL 1080  
 DB 1021 FHQQWQKNPFFLRVISDTASLCYSILKAKNAGMSIAGKGAAGPLPSEAYOWLCHOAFL 1080

QY 1081 KLTRHRVTTYVPLGSLRTAQTLRSRKLPGTTLTALEAAANPALPSDFKTLID 1132  
 DB 1081 KLTRHRVTTYVPLGSLRTAQTLRSRKLPGTTLTALEAAANPALPSDFKTLID 1132

RESULT 9  
 AAB99930  
 ID AAB99930 standard; protein; 1132 AA.  
 XX  
 AC AAB99930;  
 XX  
 DT 26-SEP-2001 (First entry)  
 XX Human telomerase protein sequence SEQ ID NO:31.  
 XX  
 KW Differentiation; heart muscle cell; cytokine; transcription factor;  
 KW proliferation; surface antigen; heart disease; cardionmyocyte;  
 KW bone marrow; umbilical blood cell; heart muscle degeneration;  
 KW myocardial infarction.  
 XX  
 OS Homo sapiens.  
 PN WO200148150-A1.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 02-NOV-2000; 2000WO-JP007741.  
 XX  
 PR 28-DEC-1990; 99JP-00372826.  
 XX  
 PR 28-FEB-2000; 2000WO-JP001148.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Umezawa, A., Hata, J., Fukuda, K., Ogawa, S., Sakurada, K., Gojo, S.;  
 PI Yamada, Y.;  
 XX  
 DR WPI; 2001-425655/45.  
 DR N-PSDB; AAI44366.  
 XX  
 PT Cells capable of differentiating into cardionmyocytes and originating in  
 PT bone marrow or umbilical blood cells for study of cardionmyocyte  
 PT differentiation and treatment of heart disease.  
 XX  
 PS Claim 146; Page 137-141; 187pp; Japanese.

CC The present invention describes cells originating in bone marrow or  
 CC umbilical blood cells which are capable of differentiating into  
 CC cardionmyocytes. Also described are: (1) cardionmyocytes produced by the  
 CC differentiation of the cells; (2) a method for carrying out the  
 CC differentiation into cardionmyocytes, regulated by a promotional and/or  
 CC inhibitory factor; (3) a method for the differentiation of the cells into  
 CC cell types other than cardionmyocytes; (4) drug compositions promoting the  
 CC formation of heart muscle and regeneration of heart tissue which contain  
 CC the cells; (5) a method for the production of antibodies which recognise  
 CC the cells, especially antibodies which recognise a surface antigen on the  
 CC cells; (6) a method for screening factors which promote the proliferation  
 CC of the cells; (7) a method for immortalising the cells by expressing  
 CC telomerase in them; (8) drug compositions for the treatment of heart  
 CC disease which contain the immortalised cells; and (9) cell-free  
 CC supernatant from the culture of the cells and its use in promoting their  
 CC differentiation into cardionmyocytes. The cells are used in the treatment  
 CC of diseases involving heart muscle degeneration, such as myocardial  
 CC infarction and in the study of cardionmyocyte differentiation. AAI44351 to  
 CC AAB99935 and AAB99915 to AAB99935 represent sequences used in the  
 CC specification of the present invention  
 XX Sequence 1132 AA;  
 SQ Query Match 100.0%; score 5961; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPCRATVSLRSHYREVLPAFVRLGPQFWRLVQGDPAFRALVACQCLVCPW 60  
 DB 1 MPRAPCRATVSLRSHYREVLPAFVRLGPQFWRLVQGDPAFRALVACQCLVCPW 60

QY 61 DARRPPAAPSFRQVSCLKEVARYLQRLCERGAKNVLAFCFALDARGGPPPEATTTSVR 120  
 DB 61 DARRPPAAPSFRQVSCLKEVARYLQRLCERGAKNVLAFCFALDARGGPPPEATTTSVR 120

QY 121 SYLPNTVTDALRGSAWGLLRLRGGDVLVHLLARCALFWLVASCAVQVCPYIQLGA 180  
 DB 121 SYLPNTVTDALRGSAWGLLRLRGGDVLVHLLARCALFWLVASCAVQVCPYIQLGA 180

QY 181 ATQARPPPHASGPPRLGERAWHNSVREAGVPLPGLPAPARRGGSASRLSPPKRPRR 240  
 DB 181 ATQARPPPHASGPPRLGERAWHNSVREAGVPLPGLPAPARRGGSASRLSPPKRPRR 240

QY 241 GAAPPERTVQGGSWAHPGRTGSPDRGFCVWSPARPAEATLEGALSGTRSHPSVG 300  
 DB 241 GAAPPERTVQGGSWAHPGRTGSPDRGFCVWSPARPAEATLEGALSGTRSHPSVG 300

QY 301 RQHAGGPPSTSRRPPWDTPCPYPAETHFLYSGDKEOLRSPFLSSLRSPGTGARRL 360  
 DB 301 RQHAGGPPSTSRRPPWDTPCPYPAETHFLYSGDKEOLRSPFLSSLRSPGTGARRL 360

QY 361 VETITLGSRWMPGPTRPLPDRYWMPGPTRPLPDRYWMPGPTRPLPDRYWMPGPTRPLW 420  
 DB 361 VETITLGSRWMPGPTRPLPDRYWMPGPTRPLPDRYWMPGPTRPLW 420

QY 421 PAAGTCAREKPGQSYAAPEEEDTPRRLVQLRQHSSPQVYGYTRACLRPLVPPGLWGS 480  
 DB 421 PAAGTCAREKPGQSYAAPEEEDTPRRLVQLRQHSSPQVYGYTRACLRPLVPPGLWGS 480

QY 481 RHNERFLRNTKKFISLGKHAKLSQLELTWMSRDCAMLRSRSPGVCVPAAEHLREEI 540  
 DB 481 RHNERFLRNTKKFISLGKHAKLSQLELTWMSRDCAMLRSRSPGVCVPAAEHLREEI 540

QY 541 LAKFJHMLSVVYELLRSFVYETTFOQNRLFYRKSYWSKQSIGRQLKRVQLRE 600  
 DB 541 LAKFJHMLSVVYELLRSFVYETTFOQNRLFYRKSYWSKQSIGRQLKRVQLRE 600

QY 601 LSEAEVROHREARPALITSRLRFPKPDGLRPIVNMDDYVGAERTREKAEILTSRVKA 660  
 DB 601 LSEAEVROHREARPALITSRLRFPKPDGLRPIVNMDDYVGAERTREKAEILTSRVKA 660

QY 661 LFSVINYERARRPGLGASVYGLDDIHRRAWTFLVRVRAQDPPLPFLYKVDTGAYDTI 720  
 DB 661 LFSVINYERARRPGLGASVYGLDDIHRRAWTFLVRVRAQDPPLPFLYKVDTGAYDTI 720

QY 721 PQDRTEVIASTIIPQNTCYVRAVQVKAHGHYRKAFSKHVSVLTDQPYMRFV AHL 780  
 DB 721 PQDRTEVIASTIIPQNTCYVRAVQVKAHGHYRKAFSKHVSVLTDQPYMRFV AHL 780

QY 781 QETSPRLDAVIEQSSSLNEASSGLFDVPLRMCHAVIRGSKYVQCGQIPOGSSILSTL 840  
 DB 781 QETSPRLDAVIEQSSSLNEASSGLFDVPLRMCHAVIRGSKYVQCGQIPOGSSILSTL 840

QY 841 LCSLCYGDMEALKFAGIRRGLLRLVDDFLVTPHLTHAKTFRLVRCVPEYGCVVLN 900  
 DB 841 LCSLCYGDMEALKFAGIRRGLLRLVDDFLVTPHLTHAKTFRLVRCVPEYGCVVLN 900

QY 901 RKTVNPFVDEALGGTAFVOMPHGLFPWCGLILDTTRLEQSDYSSSTARTSRSATLTF 960  
 DB 901 RKTVNPFVDEALGGTAFVOMPHGLFPWCGLILDTTRLEQSDYSSSTARTSRSATLTF 960

QY 961 NRGPKAGRMRRKLUFLKCHSLFLDQVNISLQTCVCMNIYKILLQAYRFHACVYQLP 1020  
 DB 961 NRGPKAGRMRRKLUFLKCHSLFLDQVNISLQTCVCMNIYKILLQAYRFHACVYQLP 1020

QY 1021 FHOQYWNPNPFLRVTISDTSLCLYSILKAKNAGMSLGAQGAQPLPSEAVQWLCHQAFLL 1080

Db	1021	FHQQVWNKPFFLVRVISDTASLCYSILKAKNAGNSLGIKGAAGPLPSSAVQWLCHQAFILL	1080	FT	Peptide	FT	Peptide	/note= "HLA-A2.1 binding motif" 883. .891
OY	1081	KLTRHRVTVPLLGSLRATQTLQSRKLPGNTLTALEAAANPALSDFKFTILD	1132	FT	Peptide	FT	Peptide	/note= "HLA-A2.1 binding motif" 926. .934
Db	1081	KLTRHRVTVPLLGSLRATQTLQSRKLPGNTLTALEAAANPALSDFKFTILD	1132	FT	Peptide	FT	Peptide	/note= "HLA-A2.1 binding motif" 934. .942
<b>RESULT 10</b>								
AAB2765	AAB2765	standard; protein; 1132 AA.		FT	Peptide	FT	Peptide	/note= "HLA-A2.1 binding motif" 969. .977
XX	AAB2765;			FT	Peptide	FT	Peptide	/note= "HLA-A2.1 binding motif" 988. .996
AC				FT	Peptide	FT	Peptide	/note= "HLA-A2.1 binding motif" 1072. .1080
XX				FT	Peptide	FT	Peptide	/note= "HLA-A2.1 binding motif" 1079. .1087
DT	29-OCT-2001	(first entry)		FT	Peptide	FT	Peptide	/note= "HLA-A2.1 binding motif" 1095. .1103
XX	Human telomerase reverse transcriptase.			FT	Peptide	FT	Peptide	/note= "HLA-A2.1 binding motif" 1122. .1130
DE	XX	telomerase reverse transcriptase; hTRT; human; cancer; tumour;		FT	Peptide	FT	Peptide	/note= "HLA-A2.1 binding motif" XX
KW	cytotoxic T lymphocyte; major histocompatibility complex;			PN	WO20010391-A1.			
KW	human leucocyte antigen; HLA-A2.1; vaccine.			XX				
XX				XX				
OS	Homo sapiens.			XX				
XX				XX				
FH		Location/Qualifiers		XX				
FT	Peptide	13. .21		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	23. .31		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	76. .84		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	96. .104		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	140. .148		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	152. .160		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	346. .354		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	353. .361		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	371. .379		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	388. .396		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	407. .415		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	487. .495		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	547. .548		XX				
FT	Peptide	/label= p540		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	548. .556		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	555. .563		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	572. .580		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	705. .713		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	724. .732		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	772. .780		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	797. .805		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	812. .820		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	836. .844		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	863. .871		XX				
FT	Peptide	/note= "HLA-A2.1 binding motif"		XX				
FT	Peptide	865. .873		XX				
		/label= P865		SQ	Sequence 1132 AA;			
				Query	Match 100.0%	Score 5961;	DB 4;	Length 1132;
				Best Local Simillarity	100.0%	Pred. No. 0;	Indels 0;	Gaps 0;
				Matches	1132;	Conservative 0;	Mismatches 0;	





Db	3.61	VETIFLGSRPRMPGTPRPLPRLPQRYWQMRPLFELIGNHAQCPYGVLKTHCPRAAVT	420	PF 16-OCT-2002; 2002W0-US033065.
QY	4.21	PAAGVCAREKQGVAPEEEDTDPRLVQLLQRISSPWOVYGFYRACURRLVPGLGWS	480	XX 22-OCT-2001; 2001US-0345326P.
Db	4.21	PAAGVCAREKQGVAPEEEDTDPRLVQLLQRISSPWOVYGFYRACURRLVPGLGWS	480	PR 20-FEB-2002; 2002US-0359196P.
QY	4.81	RHNERFLRNTKPKFISIGKHAKLSQLQETWNKMSYRDCAWLRRSPGVCUPAAEHLREEI	540	PR 22-MAY-2002; 2002US-0383195P.
Db	4.81	RHNERFLRNTKPKFISIGKHAKLSQLQETWNKMSYRDCAWLRRSPGVCUPAAEHLREEI	540	XX (UYRP ) UNIV ROCHESTER.
QY	5.41	LAKPLHILMSYVVELLRSFFVYVTTETTQKNRLFFYRKSWKSLQIGTRQHLKRVQLRE	600	XX Rowley PT;
Db	5.41	LAKPLHILMSYVVELLRSFFVYVTTETTQKNRLFFYRKSWKSLQIGTRQHLKRVQLRE	600	XX DR WPI; 2003-403336/38.
QY	6.01	LSEAEVTRQHREARPALITSRURFPIKPGDLPPIVNDYVGARTRREKAERLTSRVA	660	XX N-PSDB; ACC5839.
Db	6.01	LSEAEVTRQHREARPALITSRURFPIKPGDLPPIVNDYVGARTRREKAERLTSRVA	660	XX DR
QY	6.61	LFSVINYERARRPGLIGASVIGLDDIHRANTRTEVLRVRAQDPPPELYFVKVDTGAYDTI	720	XX Novel double-stranded short interfering RNA having sense and antisense nucleic acids which are complementary to each other and to target nucleic acid e.g., telomerase RNA or mRNA encoding telomerase reverse transcriptase.
Db	6.61	LFSVINYERARRPGLIGASVIGLDDIHRANTRTEVLRVRAQDPPPELYFVKVDTGAYDTI	720	XX Disclosure: Fig 4; 37pp; English.
QY	7.21	PQDRLTEVIASIKPONTYCVRAYVQRAAHGHYRKAFKSHVSTLTDLOPYMQFVAHL	780	XX The present sequence is the protein sequence of human telomerase reverse transcriptase (TERT). The invention relates to the discovery that double-stranded interfering RNAs, such as short interfering RNAs (siRNA), which target telomerase RNA or TERT mRNA are capable of inhibiting telomerase activity. Inhibition of telomerase in cancer cells leads to telomere shortening, and to end chromosomal fusion, and apoptosis. Interference of telomerase activity can also be used for treatment of infertility, for contraception or sterilisation, for immunosuppression, for treatment of yeast, parasitic and fungal infections, and in antiinflammatory therapies.
Db	7.21	PQDRLTEVIASIKPONTYCVRAYVQRAAHGHYRKAFKSHVSTLTDLOPYMQFVAHL	780	XX As telomerase is active in a limited number of cell types, e.g. tumour cells, germline cells, certain stem cells of the haematopoietic system, T and B cells, sun-damaged skin, and proliferative cervix, most normal cells are not affected by telomerase RNA interference.
QY	7.81	QETSPURDAVTEQSSSLNEASSGLDFVRFMCHAVRTRGKSTVQCCQIPQGSISITL	840	XX Sequence 1132 AA;
Db	7.81	QETSPURDAVTEQSSSLNEASSGLDFVRFMCHAVRTRGKSTVQCCQIPQGSISITL	840	Query Match 100.0%; Score 5961; DB 6; Length 1132;
QY	8.41	LCSLCYGDMDENKLFAGIRRQDGLLRLVDDFLVPHLTHAKTFLRLVNGVPEYGCVNL	900	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Db	8.41	LCSLCYGDMDENKLFAGIRRQDGLLRLVDDFLVPHLTHAKTFLRLVNGVPEYGCVNL	900	Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	9.01	RKTVDNFPVDEBALGCTAFTQMPANGLPPWGLLDTDTLEVQSDYSSTARTSIRASLTF	960	QY 1 MPRAPRCRAVRSLLRSHYREVLPATIYFVRLGPQGWRLVQRGDAAFRALVAQCLVCPW 60
Db	9.01	RKTVDNFPVDEBALGCTAFTQMPANGLPPWGLLDTDTLEVQSDYSSTARTSIRASLTF	960	Db 1 MPRAPRCRAVRSLLRSHYREVLPATIYFVRLGPQGWRLVQRGDAAFRALVAQCLVCPW 60
QY	9.61	NRGFKAGRNNMERKLFGVLRKCHSFLDLOVNSLOTCNTYKILLQAYTRFHACVYQLP	1020	QY 1 DARRPPAAASFQOVSCLKEVARYLQRLCERGANKVLAQFLGARDGPPFEFTSVR 120
Db	9.61	NRGFKAGRNNMERKLFGVLRKCHSFLDLOVNSLOTCNTYKILLQAYTRFHACVYQLP	1020	Db 1 DARRPPAAASFQOVSCLKEVARYLQRLCERGANKVLAQFLGARDGPPFEFTSVR 120
QY	10.21	PHQQWIKNPKTFRLVISTDTASLCYSTLAKAKNAGMSIGAKGAAGPLPSEAVOWLCHQAFIL	1080	QY 61 SYLPNTVTDALRGSGAWGGLLRLVYQDDVYLHLLARCALFVLYVAPSCAYQVCGPPLYQLGA 180
Db	10.21	PHQQWIKNPKTFRLVISTDTASLCYSTLAKAKNAGMSIGAKGAAGPLPSEAVOWLCHQAFIL	1080	Db 61 SYLPNTVTDALRGSGAWGGLLRLVYQDDVYLHLLARCALFVLYVAPSCAYQVCGPPLYQLGA 180
QY	10.81	KLTTRHRTVTTPLGSLRSTAQTQSLRKLPGTGTTALEAANPALPFDKTLD 1132	1132	QY 121 SYLPNTVTDALRGSGAWGGLLRLVYQDDVYLHLLARCALFVLYVAPSCAYQVCGPPLYQLGA 180
Db	10.81	KLTTRHRTVTTPLGSLRSTAQTQSLRKLPGTGTTALEAANPALPFDKTLD 1132	1132	Db 121 SYLPNTVTDALRGSGAWGGLLRLVYQDDVYLHLLARCALFVLYVAPSCAYQVCGPPLYQLGA 180
QY	11-AUG-2003	(First entry)		QY 181 ATQARPPPHASGPRLGCERAWNHSVREAGVPLGLPAGARRGGSASRSLPLPKRPRR 240
XX		Human telomerase reverse transcriptase.		Db 181 ATQARPPPHASGPRLGCERAWNHSVREAGVPLGLPAGARRGGSASRSLPLPKRPRR 240
AC	ABR4.2384;			QY 241 GAAPPPEPFPVGQSSWAHPTRGSDRCPVCSYPARPABEATLEGALGTRISHPSVG 300
XX				Db 301 ROHHAGPPSTSRPRPWPDTCPYPAETKHFYSSGDKEOLRPSFLSSLRSPSLTGARRL 360
DT				Db 301 ROHHAGPPSTSRPRPWPDTCPYPAETKHFYSSGDKEOLRPSFLSSLRSPSLTGARRL 360
DE				QY 301 VETIFLGSRPRMPGTPRRLPLPQRYWQMRPLFELIGNHAQCPYGVLKTHCPRLRAAVT 420
XX				XX (UYRP ) UNIV ROCHESTER.
KW		Telomerase reverse transcriptase; TERT; enzyme; RNA interference;		QY 361 VETIFLGSRPRMPGTPRRLPLPQRYWQMRPLFELIGNHAQCPYGVLKTHCPRLRAAVT 420
KW		short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;		XX (UYRP ) UNIV ROCHESTER.
KW		immunosuppressive; antiinflammatory; fungicide; antiparasitic;		QY 361 VETIFLGSRPRMPGTPRRLPLPQRYWQMRPLFELIGNHAQCPYGVLKTHCPRLRAAVT 420
KW		antiinflammatory; human; gene therapy.		XX (UYRP ) UNIV ROCHESTER.
OS		Homo sapiens.		QY 421 PAAGYCAREKPGQSYVAAPBBDTQPRRLVQLLQHSSPMQVYGVTRACURRLVPGLGWS 480
XX				Db 421 PAAGYCAREKPGQSYVAAPBBDTQPRRLVQLLQHSSPMQVYGVTRACURRLVPGLGWS 480
PD				QY 481 RHNRERFLRNTKPKFTSLGKHAKLSQLETWMSTYRDCAWLURRSSPGVCAEHLREEI 540
XX				

Db	481 RANERRFLRNTKXPFISLGKHAKLSQLSLTWMNSVRDCAWLRRSPGVGCVPAAEHLRBEI	540	PI Rowley PT; XX
Qy	541 LAKFLHNMSSYYVVELLRSFFTYTETTEFKNRLLFFYRKSTWSKLQSIGIQLKRVQRE	600	WPI; 2003 403289/34. DR
Db	541 LAKFLHNMSSYYVVELLRSFFTYTETTEFKNRLLFFYRKSTWSKLQSIGIQLKRVQRE	600	N-PSDB; ACC57552. DR
Qy	601 LSEAEVHQREARPALITSURFPIPKEDGLRPIVANDYVWGARTERKERAERLTSRVA	660	XX Novel nucleic acid encoding or comprising interfering RNAs which target telomerase RNA, useful for inhibiting telomerase activity for treating cancer, infertility and disorders of the immune system.
Db	601 LSEAEVHQREARPALITSURFPIPKEDGLRPIVANDYVWGARTERKERAERLTSRVA	660	XX Disclosure; Fig 4; 52pp; English.
Qy	661 LFSVLNTERARRPGLIGASVGLDDIHRWTFVLRVRAODPPPELYFVKDVTGAYDTI	720	XX The present sequence is that of human telomerase reverse transcriptase (RT-RT). The invention relates to the discovery that double-stranded interfering RNAs, such as short interfering RNAs (siRNA), which target telomerase RNA or TERT RNA are capable of inhibiting telomerase activity. Inhibition of telomerase in cancer cells leads to telomere shortening, end-to-end chromosomal fusion and apoptosis. Interference of telomerase activity can also be used for treatment of infertility, for contraception or sterilisation, for immunosuppression, for treatment of yeast, parasite and fungal infections, and in anti-inflammatory therapies.
Db	661 LFSVLNTERARRPGLIGASVGLDDIHRWTFVLRVRAODPPPELYFVKDVTGAYDTI	720	XX As telomerase is active in a limited number of cell types, e.g. tumour cells, germine cells, certain stem cells of the haematopoietic system, T cells and B cells, sun-damaged skin, and proliferative cervix, most normal cells are not affected by telomerase RNA interference therapy
Qy	721 PDRRLTVIASLIKPKNTYCYVRYAVVQKAAGHRYKAFSHVSTLTDIQPYMRQFVAIL	780	XX Sequence 1132 AA;
Db	721 PDRRLTVIASLIKPKNTYCYVRYAVVQKAAGHRYKAFSHVSTLTDIQPYMRQFVAIL	780	Query Match 100.0%; Score 5961; DB 6; Length 1132; Best Local Similarity 100.0%; Pred. No. 0; Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	781 QETSPRLDAYVLEQSSSLNEASSGLDPELRFMCHAVRTRGKSYVQCCGIPQGSILSTL	840	Qy 1 MPRAPRCAVRSLRSHYREVPLATEVRLRGPOQWRLVORGDPAAFRALVAQCLVCPW 60
Db	781 QETSPRLDAYVLEQSSSLNEASSGLDPELRFMCHAVRTRGKSYVQCCGIPQGSILSTL	840	Db 1 MPRAPRCAVRSLRSHYREVPLATEVRLRGPOQWRLVORGDPAAFRALVAQCLVCPW 60
Qy	841 LCSLCYGDMDMENKLFAIGIRRDGLLRLYDFLLVTPLHATHAKTFLRLTVRGVPEYGCVNL	900	Qy 61 DARPPPAAPSPRQVSCLKELYARVLQLCERGAKNVLAEGFALLDARGGPPEAFTTSVR 120
Db	841 LCSLCYGDMDMENKLFAIGIRRDGLLRLYDFLLVTPLHATHAKTFLRLTVRGVPEYGCVNL	900	Db 61 DARPPPAAPSPRQVSCLKELYARVLQLCERGAKNVLAEGFALLDARGGPPEAFTTSVR 120
Qy	901 RKTVVFNPVDEBALGATCAFQMPAIGLFDLQVNSLQTYCNIYKILLQYRPHACVULP	960	Qy 121 SYLPLNTVTDALRGSGAWGLLRLVHLLARCALFVLLVAPSCAYQVGPPLVQLGA 180
Db	901 RKTVVFNPVDEBALGATCAFQMPAIGLFDLQVNSLQTYCNIYKILLQYRPHACVULP	960	Db 121 SYLPLNTVTDALRGSGAWGLLRLVHLLARCALFVLLVAPSCAYQVGPPLVQLGA 180
Qy	961 NRGPKAGRNMWRKLPGSVLRLKCHSLFLDLQVNSLQTYCNIYKILLQYRPHACVULP	1020	Qy 1.81 ATQARPPPHASPRRLIGCERAWNHSVREACVPLGLPAPGARRRGCASRSLPLPKRPRR 240
Db	961 NRGPKAGRNMWRKLPGSVLRLKCHSLFLDLQVNSLQTYCNIYKILLQYRPHACVULP	1020	Db 1.81 ATQARPPPHASPRRLIGCERAWNHSVREACVPLGLPAPGARRRGCASRSLPLPKRPRR 240
Qy	1021 FHQQWKNPNTPLRVTISATSLCKSILRAKAGNMSLGAKGAAGPLSEAVQWILQHQAFTL	1080	Qy 241 GAAPEPRTPYQGGSWAHPGRTRGSDRGFCVVSAPPAREATSLLEGALSGTRHSHPSVG 300
Db	1021 FHQQWKNPNTPLRVTISATSLCKSILRAKAGNMSLGAKGAAGPLSEAVQWILQHQAFTL	1080	Db 241 GAAPEPRTPYQGGSWAHPGRTRGSDRGFCVVSAPPAREATSLLEGALSGTRHSHPSVG 300
Qy	1081 KLTRHRTVYVPLGSLRATQQLSRKLPGTTLTALEAAANPALPSDFKTLID	1132	Qy 301 RQHHAGPSTSRRPSPWDTCPVYAEKFLYSSGDKBOLRSPSLSSRPSL7GARRL 360
Db	1081 KLTRHRTVYVPLGSLRATQQLSRKLPGTTLTALEAAANPALPSDFKTLID	1132	Db 301 RQHHAGPSTSRRPSPWDTCPVYAEKFLYSSGDKBOLRSPSLSSRPSL7GARRL 360
Qy	1132	Qy 361 VETIFLGSRPMGPGRPLPQYQWQMPFLFELGNEAQCPCGVLLKTHCPRAAVT 420	
Db	1132	Db 361 VETIFLGSRPMGPGRPLPQYQWQMPFLFELGNEAQCPCGVLLKTHCPRAAVT 420	
Qy	421 PAAGTCAREKPKGSVAAPEEEEDTDPRLYVLLRHOSSPQYGYFTRACLRLVPGPLWGS	480	Qy 421 PAAGTCAREKPKGSVAAPEEEEDTDPRLYVLLRHOSSPQYGYFTRACLRLVPGPLWGS
Db	421 PAAGTCAREKPKGSVAAPEEEEDTDPRLYVLLRHOSSPQYGYFTRACLRLVPGPLWGS	480	Db 421 PAAGTCAREKPKGSVAAPEEEEDTDPRLYVLLRHOSSPQYGYFTRACLRLVPGPLWGS
Qy	481 RHNERFLRSTTKFSLGKHAKLSQLELTWKMSVRDCANLRRSPVGCVPAAEHLRREEI	540	Qy 481 RHNERFLRSTTKFSLGKHAKLSQLELTWKMSVRDCANLRRSPVGCVPAAEHLRREEI 540
Db	481 RHNERFLRSTTKFSLGKHAKLSQLELTWKMSVRDCANLRRSPVGCVPAAEHLRREEI	540	Qy 541 LAKFLHNMSSYYVVELLRSFFTYTETTEFKNRLLFFYRKSYWSKLQSIGIQLKRVQRE 600
Qy	541 LAKFLHNMSSYYVVELLRSFFTYTETTEFKNRLLFFYRKSYWSKLQSIGIQLKRVQRE	600	Db 541 LAKFLHNMSSYYVVELLRSFFTYTETTEFKNRLLFFYRKSYWSKLQSIGIQLKRVQRE 600
Db	541 LAKFLHNMSSYYVVELLRSFFTYTETTEFKNRLLFFYRKSYWSKLQSIGIQLKRVQRE	600	PA (TYRP ) UNIV ROCHESTER.
Qy	601 LSEAVRQHREARPALITSURFPIPKEDGLRPIVANDYVWGARTERKERAERLTSRVA	660	XX

661	LSEABVRQHREARPAALLTRLRFPKPDGLRPIVMDYVGARFRREAAELTSRVKA	660
661	LFSVNLAYERARRPGILGASVLGLDDIHRRAWTRFVLRVRAQDPPPELYFVKVDYTGAYDTI	720
661	LFSVNLAYERARRPGILGASVLGLDDIHRRAWTRFVLRVRAQDPPPELYFVKVDYTGAYDTI	720
721	PODRTEVIAISIKPQNTYCVRRAVVOQAAGHVRKAPKSHVSTLTDLQPYMRQFV AHL	780
721	PODRTEVIAISIKPQNTYCVRRAVVOQAAGHVRKAPKSHVSTLTDLQPYMRQFV AHL	780
781	QETSPILRDAVIEQSSSLNEAASSGIFDVPLRPMCHAVIRGKSYVQCCG1PQSSILSTL	840
781	QEISPLRDAVIEQSSSLNEAASSGIFDVPLRPMCHAVIRGKSYVQCCG1PQSSILSTL	840
841	LCSLGYGDMEKLFAGIRRDGLLRLVDDFLLYTPHLTHAKTFLRTRLYRGVPEYGCVNLL	900
841	LCSLGYGDMEKLFAGIRRDGLLRLVDDFLLYTPHLTHAKTFLRTRLYRGVPEYGCVNLL	900
901	RKTYVNFYVDEAALGGTAVQMPAHGLFPWCGLJLDTTRLEQSYDSSYSTARTSTRASLTF	960
901	RKTYVNFYVDEAALGGTAVQMPAHGLFPWCGLJLDTTRLEQSYDSSYSTARTSTRASLTF	960
961	NRGPKAAGRNNRRLKEFLGVLRLKCHS1FLDQVNSLQTVCTN1YKLILLQAYRFHVCLQLP	1020
961	NRGPKAAGRNNRRLKEFLGVLRLKCHS1FLDQVNSLQTVCTN1YKLILLQAYRFHVCLQLP	1020
1021	FHQCYWKNPTEFLRVTSDFASLCYSLKAKNAGNMSLGAKGAAGPLPSBAYQWLCQAFLL	1080
1021	FHQCYWKNPTEFLRVTSDFASLCYSLKAKNAGNMSLGAKGAAGPLPSBAYQWLCQAFLL	1080
1081	KLTHRHRTYVPLGSLRTAQTOLSRKLPKPTTIALEAAANPAPSDPFTKLLD	1132
1081	KLTHRHRTYVPLGSLRTAQTOLSRKLPKPTTIALEAAANPAPSDPFTKLLD	1132

TESTRESULT 15  
BBP56676 ARP56676 standard: protein: 1132 AA

ABP56676;  
25-MAR-2003 (First entry)  
Human telomerase reverse transcriptase protein SEQ ID NO:2

11

WO200291999-A2.  
21-NOV-2002.  
09-MAY-2002: 20002WO-IISO14

09-MAY-2001; 2001US-0289903P.  
(GERO-) GERON CORP.  
Tianq X Chiu C Harlev CB.

WPI: 2003-120591/11.

Composition for treating wounds and enhancing epithelialization of a skin surface, comprises vector encoding telomerase reverse transcriptase or

Disclosure: Page 32: 600pp; English.

601 LSEAEVROHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTTERKERAERLTSRVKA 660

The present invention describes a pharmaceutical composition (I) comprising a vector encoding telomerase reverse transcriptase (TERT) in an excipient or device, or comprises telomered epithelial cells on a microparticle or a matrix suitable for topical administration or administration to a wound site. (I) has vulnery and antulcer activities and can be used to promote epithelial cell migration. (I) is useful for treating a wound and enhancing epithelialisation of a skin surface. The wound is especially skin wound including acute lesion such as traumatic lesion, burn, or surgical incision, chronic lesion such as chronic venous ulcer, diabetic ulcer or compression ulcer and the wound is further monitored for closure. The telomerase activity or TERT expression is increased in epithelial cells at the site of treatment and also in fibroblasts or endothelial cells at the site of treatment. The epithelial cells are especially keratinocytes. A polynucleotide encoding TERT is useful for the preparation of a medicament for treatment of a wound or an epithelial surface in a human or animal. An epithelial cell with increased telomerase activity or increased expression of TERT is useful for preparation of a medicament for the treatment of a wound in a human or animal. (I) is also useful for treating wounds of other epidermal surfaces including mucosal surfaces such as bronchus, mouth, nose, oesophagus, stomach, or intestine. The present sequence represents human TERT (hTERT), which is given in the exemplification of the present invention. hTERT is located to chromosome 5 Sequence 1132 AA;

1	MPRAPRCAVRSLLRSHYREVPLATFVRLLPGPOWRLLYQRGDPAAFRALVAQCIVCPV	60
1	MPRAPRCAVRSLLRSHYREVPLATFVRLLPGPOWRLLYQRGDPAAFRALVAQCIVCPV	60
61	DARPPAAFSFQVSCLKELVQLCERGATKVLALFGFALLDARGCPEPENFTTSVR	120
61	DARPPAAFSFQVSCLKELVQLCERGATKVLALFGFALLDARGCPEPENFTTSVR	120
121	SYLPNTVTDALRGSGAWGLLRLRGDDLVLLARCALPLVAPSCAYQVCPPLYQLGA	180
121	SYLPNTVTDALRGSGAWGLLRLRGDDLVLLARCALPLVAPSCAYQVCPPLYQLGA	180
181	ATOAPPAPHASGPRLGGERAHHNSVREAGVPLGLPAPGARRGGSARSLSLPLPKRPRR	240
181	ATQAPPAPHASGPRLGGERAHHNSVREAGVPLGLPAPGARRGGSARSLSLPLPKRPRR	240
241	GAAPPERTPVGQSSWAHPGTRTSDRGPCTPQVYAEKHFLYSSGDKSQRPSFLSSLRPLSTGARRL	300
241	GAAPPERTPVGQSSWAHPGTRTSDRGPCTPQVYAEKHFLYSSGDKSQRPSFLSSLRPLSTGARRL	300
301	RQHAGPPSTSRSRPRPMDTPCPYVAAETKHFLYSSGDKSQRPSFLSSLRPLSTGARRL	360
301	RQHAGPPSTSRSRPRPMDTPCPYVAAETKHFLYSSGDKSQRPSFLSSLRPLSTGARRL	360
361	VETIFLGSRPMMPCTPRLPRLPQYQWQMRPLFLLELGNHAQCPYGVLLKTHCPRAAVT	420
361	VETIFLGSRPMMPCTPRLPRLPQYQWQMRPLFLLELGNHAQCPYGVLLKTHCPRAAVT	420
421	PAAGUCAREPKQGSAAPEEEEDTDRLLVQLRHOSSPMQVYGPTRACURRLVPGLGWS	480
421	PAAGUCAREPKQGSAAPEEEEDTDRLLVQLRHOSSPMQVYGPTRACURRLVPGLGWS	480
481	RHNERFLENTKETSLGKHAKLSLQELTWIMSYRDCAWLRSPVGCVPAABHLRREEI	540
481	RHNERFLENTKETSLGKHAKLSLQELTWIMSYRDCAWLRSPVGCVPAABHLRREEI	540
541	LAKFHWMNSVYVLLRSFFYTTETTFQKNRLFFYRKSYWSKLQSIGIRQLKRVOLRE	600
541	LAKFHWMNSVYVLLRSFFYTTETTFQKNRLFFYRKSYWSKLQSIGIRQLKRVOLRE	600
601	LSEAVRQREARPAALLTSLRFLPKPDGURPTIMMDYVGARTFRREGAERTSRVKA	660
601	LSEAVRQREARPAALLTSLRFLPKPDGURPTIMMDYVGARTFRREGAERTSRVKA	660

Qy	661	LFSVNLNEYERARRPGLIGASVIGLDDIHRAMRTFVLVRRAODPPBPLYFVKVDVTGAYDTI	720
Db	661	LFSVNLNEYERARRPGLIGASVIGLDDIHRAMRTFVLVRRAODPPBPLYFVKVDVTGAYDTI	720
Qy	721	PQDRLTTEVIASIIKPCONTYCVRYYAVVQKAAGHVRKAFKSHVSTLTDIOPYMRQFVAHL	780
Db	721	PQDRLTTEVIASIIKPCONTYCVRYYAVVQKAAGHVRKAFKSHVSTLTDIOPYMRQFVAHL	780
Qy	781	QETSPRDAVVIEQSSSLNEAASSGLFDVFLRMRMCHAVRIGKSYVOCQGIPQGSILSTL	840
Db	781	QETSPRDAVVIEQSSSLNEAASSGLFDVFLRMRMCHAVRIGKSYVOCQGIPQGSILSTL	840
Qy	841	LCSLCYCGDMENKLPGIRRDCLLRLVDDFLVTPHILTHAKTFPLTVGVPETGCVNLL	900
Db	841	LCSLCYCGDMENKLPGIRRDCLLRLVDDFLVTPHILTHAKTFPLTVGVPETGCVNLL	900
Qy	901	RKTVVNFPPVEDALGCTAFYQMPAHLGLFPMCGLLIDRTTLEQSDSYARTSIRASLTTF	960
Db	901	RKTVVNFPPVEDALGCTAFYQMPAHLGLFPMCGLLIDRTTLEQSDSYARTSIRASLTTF	960
Qy	961	NRGFKAGRMNMRKLGVLRLKCHSFLDIQNSLQTVCNKILLOAYRFIACVLQLP	1020
Db	961	NRGFKAGRMNMRKLGVLRLKCHSFLDIQNSLQTVCNKILLOAYRFIACVLQLP	1020
Qy	1021	PHQOTWKNPTEFLRIVSPTASLCSISLAKKAGNAGSLGAKGAAGLPSEAVQWLCHQAFIL	1080
Db	1021	PHQOTWKNPTEFLRIVSPTASLCSISLAKKAGNAGSLGAKGAAGLPSEAVQWLCHQAFIL	1080
Qy	1081	KLTRHRVTVYVPLLGSLRATQQLSRLPQTTLTALEAAANPALPSDFKTIID	1132
Db	1081	KLTRHRVTVYVPLLGSLRATQQLSRLPQTTLTALEAAANPALPSDFKTIID	1132

Search completed: January 10, 2005, 17:34:53  
 Job time : 175 secs



RA	Beattie T.L., Zhou W., Robinson M.O., Harrington L.;	Harrington L.;	PubMed:11029039;
RA	"Polymerase domain defects within human telomerase are distinct from telomerase RNA and TBP1 binding."		
RT	Mol. Biol. Cell 11:3319-3340 (2000).		
RT	-1- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for the replication of chromosome termini in most eukaryotes. It elongates telomeres. It is a reverse transcriptase that adds simple sequence repeats to chromosome ends by copying a template sequence within the RNA component of the enzyme.		
CC	-1- SUBUNIT: Component of the telomerase ribonucleoprotein complex at least composed of TEP1, EST1A, POT1 and a telomerase RNA template component (TER). Interacts with PNX1.		
CC	-1- SUBCELLULAR LOCATION: Nuclear.		
CC	-1- DISEASE: Activation of telomerase has been implicated in cell immortalization and cancer cell pathogenesis.		
CC	-1- SIMILARITY: Belongs to the reverse transcriptase family.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/or_bend_an_email_to_license@isb-sib.ch">http://www.isb-sib.ch/announce/or_bend_an_email_to_license@isb-sib.ch</a> ).		
CC	-----		
CC	EMBL; AF015950; AAC51672.1; -		
DR	AF015950; AAC51672.1; -		
DR	AF124894; AAD30037.1; -		
DR	AF124893; AAD30037.1; JOINED.		
DR	AY007685; AAG22289.1; -		
DR	PIR; T03844; T01944.		
DR	Genew; HGNC:11710; TERT.		
DR	MIM; 187270; -		
DR	GO; GO:0000781; C:chromosome, telomeric region; TAS.		
DR	GO; GO:0041162; F:telomeric DNA binding; TAS.		
DR	GO; GO:0031721; F:telomeric template RNA reverse transcriptas. . . ; TAS.		
DR	InterPro; IPR000477; RVTB.		
DR	InterPro; IPR003545; RVTB.		
DR	Pfam; PF00078; RVT; 1.		
DR	PRINTS; PR11365; TELOMERASE.		
KW	DNA-binding; Nuclear protein; Ribonucleoprotein;		
KW	RNA-directed DNA polymerase; Telomere; Transferase.		
PT	MUTAGEN	D->A: Loss of telomerase activity.	
PT	MUTAGEN	868 868 DD->AA: Loss of telomerase activity.	
PT	MUTAGEN	869 869 D->A: Loss of telomerase activity.	
PT	MUTAGEN	712 712 D->A: Loss of telomerase activity.	
PT	MUTAGEN	516 516 D->G (In Ref. 2).	
SEQUENCE	1132 AA; 126996 MW; 948354534CA33A0 CRC64;		
Query Match	100.0%; Score 5961; DB 1; Length 1132;		
Best Local Similarity	100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;		
Matches	1132; Conservative 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 MPRAPCRAVSILLSHYREVPLPLATEVRLGPQGNRLVQGDPAAFRALVAQCLVCPW	1 MPRAPCRAVSILLSHYREVPLPLATEVRLGPQGNRLVQGDPAAFRALVAQCLVCPW	Qy 1 MPRAPCRAVSILLSHYREVPLPLATEVRLGPQGNRLVQGDPAAFRALVAQCLVCPW
Db	1 MPRAPCRAVSILLSHYREVPLPLATEVRLGPQGNRLVQGDPAAFRALVAQCLVCPW	1 MPRAPCRAVSILLSHYREVPLPLATEVRLGPQGNRLVQGDPAAFRALVAQCLVCPW	Db 1 MPRAPCRAVSILLSHYREVPLPLATEVRLGPQGNRLVQGDPAAFRALVAQCLVCPW
Qy	61 DARPPRPPAPSPQQVSCIKELLYARVQLCERGAKNVLAEGFSLILDARGGGPEAFTSVR	61 DARPPRPPAPSPQQVSCIKELLYARVQLCERGAKNVLAEGFSLILDARGGGPEAFTSVR	Qy 61 DARPPRPPAPSPQQVSCIKELLYARVQLCERGAKNVLAEGFSLILDARGGGPEAFTSVR
Db	61 DARPPRPPAPSPQQVSCIKELLYARVQLCERGAKNVLAEGFSLILDARGGGPEAFTSVR	61 DARPPRPPAPSPQQVSCIKELLYARVQLCERGAKNVLAEGFSLILDARGGGPEAFTSVR	Db 61 DARPPRPPAPSPQQVSCIKELLYARVQLCERGAKNVLAEGFSLILDARGGGPEAFTSVR
Qy	121 SYLPLNFTDARGSGAWGLLRRGDDVVLVHLLARCAFLVAPSCAYQVCGSPLPLYQLG	121 SYLPLNFTDARGSGAWGLLRRGDDVVLVHLLARCAFLVAPSCAYQVCGSPLPLYQLG	Qy 121 SYLPLNFTDARGSGAWGLLRRGDDVVLVHLLARCAFLVAPSCAYQVCGSPLPLYQLG
Db	121 SYLPLNFTDARGSGAWGLLRRGDDVVLVHLLARCAFLVAPSCAYQVCGSPLPLYQLG	121 SYLPLNFTDARGSGAWGLLRRGDDVVLVHLLARCAFLVAPSCAYQVCGSPLPLYQLG	Db 121 SYLPLNFTDARGSGAWGLLRRGDDVVLVHLLARCAFLVAPSCAYQVCGSPLPLYQLG
Qy	181 ATQARPPHASPGRRLGCERAWNHSREAGVPLGLPAGARRRGCSASRSLPLPKRPRR	181 ATQARPPHASPGRRLGCERAWNHSREAGVPLGLPAGARRRGCSASRSLPLPKRPRR	Qy 181 ATQARPPHASPGRRLGCERAWNHSREAGVPLGLPAGARRRGCSASRSLPLPKRPRR
Db	181 ATQARPPHASPGRRLGCERAWNHSREAGVPLGLPAGARRRGCSASRSLPLPKRPRR	181 ATQARPPHASPGRRLGCERAWNHSREAGVPLGLPAGARRRGCSASRSLPLPKRPRR	Db 181 ATQARPPHASPGRRLGCERAWNHSREAGVPLGLPAGARRRGCSASRSLPLPKRPRR
Qy	241 GAAPERTPTPQGSMWAHPGRPSDRCFCVSPARPAEATSLGALSGRHSFSPVG	241 GAAPERTPTPQGSMWAHPGRPSDRCFCVSPARPAEATSLGALSGRHSFSPVG	Qy 241 GAAPERTPTPQGSMWAHPGRPSDRCFCVSPARPAEATSLGALSGRHSFSPVG
Db	241 GAAPERTPTPQGSMWAHPGRPSDRCFCVSPARPAEATSLGALSGRHSFSPVG	241 GAAPERTPTPQGSMWAHPGRPSDRCFCVSPARPAEATSLGALSGRHSFSPVG	Db 241 GAAPERTPTPQGSMWAHPGRPSDRCFCVSPARPAEATSLGALSGRHSFSPVG
Qy	301 ROHHAGPPESTSRPWRPMTCPPTVYTAETHFLYSSGDEQQLRSPFLSSLRSPSLTGARRL	301 ROHHAGPPESTSRPWRPMTCPPTVYTAETHFLYSSGDEQQLRSPFLSSLRSPSLTGARRL	Qy 301 ROHHAGPPESTSRPWRPMTCPPTVYTAETHFLYSSGDEQQLRSPFLSSLRSPSLTGARRL
Db	301 ROHHAGPPESTSRPWRPMTCPPTVYTAETHFLYSSGDEQQLRSPFLSSLRSPSLTGARRL	301 ROHHAGPPESTSRPWRPMTCPPTVYTAETHFLYSSGDEQQLRSPFLSSLRSPSLTGARRL	Db 301 ROHHAGPPESTSRPWRPMTCPPTVYTAETHFLYSSGDEQQLRSPFLSSLRSPSLTGARRL
Qy	361 VETIFLGSRSPWMPGTPRPLPORYWQRPLPFLLELGNAQCPYGVLLKTHCPLRRAVT	361 VETIFLGSRSPWMPGTPRPLPORYWQRPLPFLLELGNAQCPYGVLLKTHCPLRRAVT	Qy 361 VETIFLGSRSPWMPGTPRPLPORYWQRPLPFLLELGNAQCPYGVLLKTHCPLRRAVT
Db	361 VETIFLGSRSPWMPGTPRPLPORYWQRPLPFLLELGNAQCPYGVLLKTHCPLRRAVT	361 VETIFLGSRSPWMPGTPRPLPORYWQRPLPFLLELGNAQCPYGVLLKTHCPLRRAVT	Db 361 VETIFLGSRSPWMPGTPRPLPORYWQRPLPFLLELGNAQCPYGVLLKTHCPLRRAVT
Qy	421 PAAGVCAREKPOGSVAAPFEDTDPRIVVOLLPOHSSPQVQGYVRACLRLLVPGLGWS	421 PAAGVCAREKPOGSVAAPFEDTDPRIVVOLLPOHSSPQVQGYVRACLRLLVPGLGWS	Qy 421 PAAGVCAREKPOGSVAAPFEDTDPRIVVOLLPOHSSPQVQGYVRACLRLLVPGLGWS
Db	421 PAAGVCAREKPOGSVAAPFEDTDPRIVVOLLPOHSSPQVQGYVRACLRLLVPGLGWS	421 PAAGVCAREKPOGSVAAPFEDTDPRIVVOLLPOHSSPQVQGYVRACLRLLVPGLGWS	Db 421 PAAGVCAREKPOGSVAAPFEDTDPRIVVOLLPOHSSPQVQGYVRACLRLLVPGLGWS
Qy	541 LAKPLHWMSSVYELLRSFFYVETTDFQRNLFFYRKSVWSKLSQSGIRQHLLKRVQLRE	541 LAKPLHWMSSVYELLRSFFYVETTDFQRNLFFYRKSVWSKLSQSGIRQHLLKRVQLRE	Qy 541 LAKPLHWMSSVYELLRSFFYVETTDFQRNLFFYRKSVWSKLSQSGIRQHLLKRVQLRE
Db	541 LAKPLHWMSSVYELLRSFFYVETTDFQRNLFFYRKSVWSKLSQSGIRQHLLKRVQLRE	541 LAKPLHWMSSVYELLRSFFYVETTDFQRNLFFYRKSVWSKLSQSGIRQHLLKRVQLRE	Db 541 LAKPLHWMSSVYELLRSFFYVETTDFQRNLFFYRKSVWSKLSQSGIRQHLLKRVQLRE
Qy	601 LSEAEVROHREARPALTSRLRFPKDGRLPRTLPVNMDDYVGARTFREKERAERTSRVKA	601 LSEAEVROHREARPALTSRLRFPKDGRLPRTLPVNMDDYVGARTFREKERAERTSRVKA	Qy 601 LSEAEVROHREARPALTSRLRFPKDGRLPRTLPVNMDDYVGARTFREKERAERTSRVKA
Db	601 LSEAEVROHREARPALTSRLRFPKDGRLPRTLPVNMDDYVGARTFREKERAERTSRVKA	601 LSEAEVROHREARPALTSRLRFPKDGRLPRTLPVNMDDYVGARTFREKERAERTSRVKA	Db 601 LSEAEVROHREARPALTSRLRFPKDGRLPRTLPVNMDDYVGARTFREKERAERTSRVKA
Qy	661 LFSVLYNTERARRPGLLGSVGLGDDDIHAWRTFVLRVRAQDPPEFLFYKUDVGTGAYDTI	661 LFSVLYNTERARRPGLLGSVGLGDDDIHAWRTFVLRVRAQDPPEFLFYKUDVGTGAYDTI	Qy 661 LFSVLYNTERARRPGLLGSVGLGDDDIHAWRTFVLRVRAQDPPEFLFYKUDVGTGAYDTI
Db	661 LFSVLYNTERARRPGLLGSVGLGDDDIHAWRTFVLRVRAQDPPEFLFYKUDVGTGAYDTI	661 LFSVLYNTERARRPGLLGSVGLGDDDIHAWRTFVLRVRAQDPPEFLFYKUDVGTGAYDTI	Db 661 LFSVLYNTERARRPGLLGSVGLGDDDIHAWRTFVLRVRAQDPPEFLFYKUDVGTGAYDTI
Qy	721 PQDLTVEYTASITKQNTYCVRYAVVOKAAGHGVRAKFKSHVSTLTDLQPMYQMRQFVAHL	721 PQDLTVEYTASITKQNTYCVRYAVVOKAAGHGVRAKFKSHVSTLTDLQPMYQMRQFVAHL	Qy 721 PQDLTVEYTASITKQNTYCVRYAVVOKAAGHGVRAKFKSHVSTLTDLQPMYQMRQFVAHL
Db	721 PQDLTVEYTASITKQNTYCVRYAVVOKAAGHGVRAKFKSHVSTLTDLQPMYQMRQFVAHL	721 PQDLTVEYTASITKQNTYCVRYAVVOKAAGHGVRAKFKSHVSTLTDLQPMYQMRQFVAHL	Db 721 PQDLTVEYTASITKQNTYCVRYAVVOKAAGHGVRAKFKSHVSTLTDLQPMYQMRQFVAHL
Qy	781 QETSPLRDAAVTEQSSLNNEASSGLFDYFLRFLMCHHAIRVGSYVQOCGIPQGSSILSTL	781 QETSPLRDAAVTEQSSLNNEASSGLFDYFLRFLMCHHAIRVGSYVQOCGIPQGSSILSTL	Qy 781 QETSPLRDAAVTEQSSLNNEASSGLFDYFLRFLMCHHAIRVGSYVQOCGIPQGSSILSTL
Db	781 QETSPLRDAAVTEQSSLNNEASSGLFDYFLRFLMCHHAIRVGSYVQOCGIPQGSSILSTL	781 QETSPLRDAAVTEQSSLNNEASSGLFDYFLRFLMCHHAIRVGSYVQOCGIPQGSSILSTL	Db 781 QETSPLRDAAVTEQSSLNNEASSGLFDYFLRFLMCHHAIRVGSYVQOCGIPQGSSILSTL
Qy	841 LCSLCYGMENKLFGIRRDLLLRFLVTPHATHAKTFRTLVRGVPEYGVVNL	841 LCSLCYGMENKLFGIRRDLLLRFLVTPHATHAKTFRTLVRGVPEYGVVNL	Qy 841 LCSLCYGMENKLFGIRRDLLLRFLVTPHATHAKTFRTLVRGVPEYGVVNL
Db	841 LCSLCYGMENKLFGIRRDLLLRFLVTPHATHAKTFRTLVRGVPEYGVVNL	841 LCSLCYGMENKLFGIRRDLLLRFLVTPHATHAKTFRTLVRGVPEYGVVNL	Db 841 LCSLCYGMENKLFGIRRDLLLRFLVTPHATHAKTFRTLVRGVPEYGVVNL
Qy	901 RKTIVNPFVDEAEGGTAFVQMPAHGFLPWCGLLDDRTLVEOSDYYSTARSSTRASLTF	901 RKTIVNPFVDEAEGGTAFVQMPAHGFLPWCGLLDDRTLVEOSDYYSTARSSTRASLTF	Qy 901 RKTIVNPFVDEAEGGTAFVQMPAHGFLPWCGLLDDRTLVEOSDYYSTARSSTRASLTF
Db	901 RKTIVNPFVDEAEGGTAFVQMPAHGFLPWCGLLDDRTLVEOSDYYSTARSSTRASLTF	901 RKTIVNPFVDEAEGGTAFVQMPAHGFLPWCGLLDDRTLVEOSDYYSTARSSTRASLTF	Db 901 RKTIVNPFVDEAEGGTAFVQMPAHGFLPWCGLLDDRTLVEOSDYYSTARSSTRASLTF
Qy	961 NRGFKAERNMRRLKGFLVRLKCHSLSFEDLQVNSLQTVCTNIKLLQYRFHACVQLQP	961 NRGFKAERNMRRLKGFLVRLKCHSLSFEDLQVNSLQTVCTNIKLLQYRFHACVQLQP	Qy 961 NRGFKAERNMRRLKGFLVRLKCHSLSFEDLQVNSLQTVCTNIKLLQYRFHACVQLQP
Db	961 NRGFKAERNMRRLKGFLVRLKCHSLSFEDLQVNSLQTVCTNIKLLQYRFHACVQLQP	961 NRGFKAERNMRRLKGFLVRLKCHSLSFEDLQVNSLQTVCTNIKLLQYRFHACVQLQP	Db 961 NRGFKAERNMRRLKGFLVRLKCHSLSFEDLQVNSLQTVCTNIKLLQYRFHACVQLQP
Qy	1021 FHQQWKNPTFFLRVVISDTASLCYSILKAKNAGMSLAKGAAPLSEAVQWLQHQAFLL	1021 FHQQWKNPTFFLRVVISDTASLCYSILKAKNAGMSLAKGAAPLSEAVQWLQHQAFLL	Qy 1021 FHQQWKNPTFFLRVVISDTASLCYSILKAKNAGMSLAKGAAPLSEAVQWLQHQAFLL
Db	1021 FHQQWKNPTFFLRVVISDTASLCYSILKAKNAGMSLAKGAAPLSEAVQWLQHQAFLL	1021 FHQQWKNPTFFLRVVISDTASLCYSILKAKNAGMSLAKGAAPLSEAVQWLQHQAFLL	Db 1021 FHQQWKNPTFFLRVVISDTASLCYSILKAKNAGMSLAKGAAPLSEAVQWLQHQAFLL
Qy	1069 AA.	PRELIMINARY;	Qy 1069 AA.
Db	OBNG46	OBNG46;	Db OBNG46;
AC	AC	AC	AC
DT	01-OCT-2002	(TRIMBLrel. 22, Created)	DT 01-OCT-2002
DT	01-OCT-2003	(TRIMBLrel. 22, Last sequence update)	DT 01-OCT-2003
DE	DE	DE	DE
GN	Name=NTERT;	Name=NTERT;	GN Name=NTERT;
OS	Homo sapiens (Human)	Homo sapiens (Human)	OS Homo sapiens (Human)
OC	Mammalia	Eutheria	OC Mammalia
OC	Bivalvia	Chordata	OC Bivalvia
NC	Cladocera	Vertebrata	NC Cladocera
NC	Crustacea	Vertebrata	NC Crustacea
NC	Hominoidea	Vertebrata	NC Hominoidea
NC	Homidae	Homidae	NC Homidae
NC	Homidae	Homidae	NC Homidae
NC	NCBI_TaxID=9606	NCBI_TaxID=9606	NC NCBI_TaxID=9606
NC	NCBI_TaxID=9606	NCBI_TaxID=9606	NC NCBI_TaxID=9606

RP	SEQUENCE FROM N.A.	QY	841 LCLSCYGDMDENKLFGAGIRRDGLLRLVDDDELLTPELTHAKTFRLTVRGVPEYGVVNL 900
RA	Hisamori H., Nagao K., Hirata H., Hikiji K., Kanamaru T.;	Db	841 LCLSCYGDMDENKLFGAGIRRDGLLRLVDDDELLTPELTHAKTFRLTVRGVPEYGVVNL 884
RL	Submitted (MAY-2002) to the EMBL/GemBank/DBJ databases.	QY	901 RKTIVNPFVDEALGGTAFQMPAHLFPNGCLLDDTTRLVEQSDYSSYARTSIRASLT
DR	EMBL; AB056287; BAC11010.1; -	Db	885 ---
DR	GO; GO:0005634; C:nucleus; IEA.	QY	960
DR	GO; GO:0003677; F:DNA binding; IEA.	Db	885 ---
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.	QY	897
DR	GO; GO:0003721; F:telomeric template RNA reverse transcriptas. . . ; IEA.	Db	897
DR	DR InterPro; IPR003454; Telomerase_RT.	QY	961 NRGFKAGRNNRRLKLFGLVLRKCHSLEFLDQVNSLQVTCNTYKILLQAVRFHACVQLQP 1020
DR	RNA-directed DNA polymerase; IPR01365; TELOMERAERT.	Db	898 NRGFKAGRNNRRLKLFGLVLRKCHSLEFLDQVNSLQVTCNTYKILLQAVRFHACVQLQP 957
KW	SEQUENCE 1069 AA; 120046 MW; BB1E77A653B1C666 CRC64;	QY	1021 FHQQWKNPTEFLRVLISDTASLCYSLKAKNAGMSLGAAGPLPSEAQWLCQHAFLL 1080
SO	Query Match 93.7%; Score 5583.5; DB 2; Length 1069;	Db	958 FHQQWKNPTEFLRVLISDTASLCYSLKAKNAGMSLGAAGPLPSEAQWLCQHAFLL 1132
Best Local Similarity 94.4%; Pred. No. 0;	Matches 0; M:matches 0;	QY	1081 KLTRHRVTVYPLLSLRTAQTSRSLKPGLTTLAEEAANPALSDFKTLID 1117
Matches 1069; Conservative 0;	1 MPRAPCRAYRSLLSHREYRVLPLATFVRLGPQGMRLVQRGDPAAPFALVAQCLVCPW 60	Db	1018 KLTRHRVTVYPLLSLRTAQTSRSLKPGLTTLAEEAANPALSDFKTLID 1069
Db	1 MPRAPCRAYRSLLSHREYRVLPLATFVRLGPQGMRLVQRGDPAAPFALVAQCLVCPW 60		
QY	61 DARPPPAAPSPRQVSCKELVARYLQRLCERGAKNVLAFQGLLQARGGPEAFTTSVR 120	Q8N6C3	RESULT 3
Db	61 DARPPPAAPSPRQVSCKELVARYLQRLCERGAKNVLAFQGLLQARGGPEAFTTSVR 120	Q8N6C3	PRELIMINARY;
QY	121 SYLPNTVTDALRGSGAWGLLRLRGGDVLVHLARCAFLVAPSCAYQVCGPPLYQIGA 180	Q8N6C3	PRT; 807 AA.
Db	121 SYLPNTVTDALRGSGAWGLLRLRGGDVLVHLARCAFLVAPSCAYQVCGPPLYQIGA 180	AC	Q8N6C3;
QY	181 ATQARPPHASGPRLGCEAWNHSVREAGVPLGLPAGPARRGGSASSSLPLPKRPRR 240	DT	01-OCT-2002 (TREMBLrel. 22, Created)
Db	181 ATQARPPHASGPRLGCEAWNHSVREAGVPLGLPAGPARRGGSASSSLPLPKRPRR 240	DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
QY	241 GAAPEPRTPTGPQGSAHGPGRTRGPDRGFCVSPARPAEATSLLEGALSCTRSHPSVG 300	DR	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Db	241 GAAPEPRTPTGPQGSAHGPGRTRGPDRGFCVSPARPAEATSLLEGALSCTRSHPSVG 300	DR	DE Beta and Gamma deletion isoform of telomerase reverse transcriptase.
QY	301 RQHHAGPPSTSRPPWDTPCPVYAAETKHFLYSSGKDEQLRPSFLLSLRPSLTGARRL 360	DR	DE transcriptase.
Db	301 RQHHAGPPSTSRPPWDTPCPVYAAETKHFLYSSGKDEQLRPSFLLSLRPSLTGARRL 360	DR	DR Name=HTERT.
QY	361 VETIFGSRPMPGTPRPLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPURAVT 420	DR	OS Homo sapiens (Human).
Db	361 VETIFGSRPMPGTPRPLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPURAVT 420	DR	OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBITaxID=9606;
QY	421 PAAGVCAREKQGSAVAAPEEETDTPPLVQLRQISSPWQYGYTRACLRLVPGWGS 480	DR	OX
Db	421 PAAGVCAREKQGSAVAAPEEETDTPPLVQLRQISSPWQYGYTRACLRLVPGWGS 480	DR	RN [1]
QY	481 RHNERRFLRNTKKF1SLGKHAKLSQLQELTWKMSVRDCAMLRSPGCVPAAEHLREB 540	DR	RP SEQUENCE FROM N.A.
Db	481 RHNERRFLRNTKKF1SLGKHAKLSQLQELTWKMSVRDCAMLRSPGCVPAAEHLREB 540	DR	RC TISSUE=Gastric cancer; Hisatomi H., Nagao K., Kanamaru T., Sumida H., Hirata H., Yamamoto M., Ra Kazumasa H.;
QY	541 LAKFELWLMSSVVELRSFVYETTETQKNRLFFYRKSTWSKLSQIGIROHLKRVQLE 600	DR	RA Submitted (JUN-2002) to the EMBL/CeNBank/DBJ databases.
Db	541 LAKFELWLMSSVVELRSFVYETTETQKNRLFFYRKSTWSKLSQIGIROHLKRVQLE 600	DR	DR AB016379; BAC11014.1; -
QY	601 LSEAETVRQHREARPALTSURFIPKDPGLRPTVNMDDYVNGARTFREKEAERLTSRVA 660	DR	DR GO:0005634; C:nucleus; IEA.
Db	601 LSEAETVRQHREARPALTSURFIPKDPGLRPTVNMDDYVNGARTFREKEAERLTSRVA 660	DR	DR GO:0003777; F:DNA binding; IEA.
QY	661 LFSVNLNYERARPGLGASVLGLDDTHRANTFVLVRQAQDPPELYFVYDVTGAYDTI 720	DR	DR GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
Db	661 LFSVNLNYERARPGLGASVLGLDDTHRANTFVLVRQAQDPPELYFVYDVTGAYDTI 720	DR	DR GO:0003721; F:telomerase template RNA reverse transcriptas. . . ; IEA.
QY	721 PQDRLTVIASIKPQNTYCVRYAVQKAAGHYRKAFKSHVSTLTDQYPMOFVAHL 780	QY	DR InterPro; IPR003545; Telomerase_RT.
Db	721 PQDRLTVIASIKPQNTYCVRYAVQKAAGHYRKAFKSHVSTLTDQYPMOFVAHL 780	Db	DR PRINTS; PR01365; TELOMERAERT.
QY	781 QETSPURDAVYEQSSSLNEASSGLFDVFLRMCMHAVTRGKSTYQCG3IPQGSTLSTL 840	QY	DR RNA-directed DNA polymerase.
Db	781 QETSPURDAVYEQSSSLNEASSGLFDVFLRMCMHAVTRGKSTYQCG3IPQGSTLSTL 840	QY	DR SEQUENCE 807 AA; 90225 MW; 199664460CE6D763 CRC64;
QY	841 LCLSCYGDMDENKLFGAGIRRDGLLRLVDDDELLTPELTHAKTFRLTVRGVPEYGVVNL 900	QY	Query Match 68.0%; Score 4052; DB 2; Length 807;
Db	841 LCLSCYGDMDENKLFGAGIRRDGLLRLVDDDELLTPELTHAKTFRLTVRGVPEYGVVNL 884	QY	Best Local Similarity 100.0%; Pred. No. 9-245; Matches 763; Conservative 0; M:matches 0; Indels 0; Gaps 0;
QY	901 RKTIVNPFVDEALGGTAFQMPAHLFPNGCLLDDTTRLVEQSDYSSYARTSIRASLT	Db	QY 1 MPRAPCRAYRSLLSHREYRVLPLATEVRLGPQGMWLRQGDPAAPFALVAQCLYCVPN 60
Db	885 ---	Db	1 MPRAPCRAYRSLLSHREYRVLPLATEVRLGPQGMWLRQGDPAAPFALVAQCLYCVPN 60
QY	960	QY	61 DARPAAAPSPRQVSLKELVARYLQRLCERGAKNVLAFQGLLQARGLDQARGPPEAFTTSVR 120
Db	885 ---	Db	61 DARPAAAPSPRQVSLKELVARYLQRLCERGAKNVLAFQGLLQARGLDQARGPPEAFTTSVR 120
QY	961 NRGFKAGRNNRRLKLFGLVLRKCHSLEFLDQVNSLQVTCNTYKILLQAVRFHACVQLQP 1020	QY	61 DARPAAAPSPRQVSLKELVARYLQRLCERGAKNVLAFQGLLQARGLDQARGPPEAFTTSVR 120
Db	898 NRGFKAGRNNRRLKLFGLVLRKCHSLEFLDQVNSLQVTCNTYKILLQAVRFHACVQLQP 957	QY	121 SYLPNTVTDALRGSGAWGLLRLRGGDVLVHLARCAFLVAPSCAYQVCGPPLYQIGA 180
QY	1021 FHQQWKNPTEFLRVLISDTASLCYSLKAKNAGMSLGAAGPLPSEAQWLCQHAFLL 1080	Db	121 SYLPNTVTDALRGSGAWGLLRLRGGDVLVHLARCAFLVAPSCAYQVCGPPLYQIGA 180
Db	958 FHQQWKNPTEFLRVLISDTASLCYSLKAKNAGMSLGAAGPLPSEAQWLCQHAFLL 1132	QY	181 ATQARPPHASGPRLGCEAWNHSVREAGVPLGLPAPGARRGGSASRSLPLPKRPRR 240
QY	1081 KLTRHRVTVYPLLSLRTAQTSRSLKPGLTTLAEEAANPALSDFKTLID 1117	Db	241 GAAPBEPERTPYQGGSWAHPGRTGSDRGEFCVSPARPAEATSLLEGALSCTRSHPSVG 300



DR	GO; GO:0016740; F:transferase activity; IEA.
GO	GO:0002278; P:RNA dependent DNA replication; IEA.
DR	InterPro; IPR000477; RVTse.
DR	InterPro; IPR003545; Telomerase_RT.
DR	Pfam; PF00078; RVT; 1.
DR	PRINTS; PR01365; TELOMERSERT.
KW	RNA-directed DNA polymerase; Transferase.
SEQUENCE	1128 AA; 128393 MW; 1D4F81249012174E CRC64;
Query Match	60.9%; Score 3628; DB 2; Length 1128;
Best Local Similarity	63.3%; Pred. No. 4.5e-218;
Matches	736; Conservative 124; Mismatches 239; Indels 64; Gaps 16;
Qy	1 MPPAPRCAVRSLLRSHYREVPLPLATEFVRLGPGQWRLVQRGDPAAFPALVAQCLVCYWP 60
Db	1 MPPAPRCAVRSLLRSHYREVPLPLATEFVRLGPGQWRLVQRGDPAAFPALVAQCLVCYWP 60
Qy	61 DARRPPAAPSQQVSCSLLKELVARYLQLRCLCEGAKAVLAEGFALLDGARGGPPRAFTTSVR 120
Db	61 DQQPPADLSF1QVQSSLLKELVARYLQLRCLCEGAKAVLAEGFALLDGARGGPPRAFTTSVR 120
Qy	121 SYLPNTVTDALRGSGAWGLLLREVGDDVLYHLLARCAFLVYLPSCAYQVCGGPPLYQLGA 180
Db	121 SYLPNTVTDALRGSGAWGMLLARCAFLVYLPSCAYQVCGGPPLYQLGA 180
Qy	181 ATQARPP -PHASGPRRLG-----CERAWNHSVREBAGVPLGLPAGARRGGSAARS 231
Db	181 TABTWPVSRYTRPGRNFTLGHSTHRVNSHQQAWKPPPLPSREAKRLSITMRS 240
Qy	232 LPLPKRBRGAADPEPRTDVGQSWAHFGTRGTRPSDRCFTCWSPAR----PABEATSLG 287
Db	241 VPPSKKARCDLAPRLKGPRYQA-----VPVTPSDKTW-VPNPAKSHAVPISRTTK-ED 291
Qy	288 ALSGTRHSHPSVGRQ---HHAGGPPSTS-RPP-----RPWDTCPBPVYASTKHFYLS 334
Db	292 LSGGVK -APGLSRSGSYCYKPKSSSTLQSPFLCQNAFQLR-----YETKRFYLS 341
Qy	335 -SGDKEQLRPSFLLRPSLTTGARRLVETITFLGSRPMPGTPRRLPRLPQRYWQMRPLF 393
Db	342 REGGRBLNPSPFLNNQQLPSLTSGARRLVBLGPMGRPTSGPGLCGRERLSSKRYWQMRPLF 401
Qy	394 LEILGNAQCPGVLLTHCPIRAATPAVGCVAREFQGSVAPEEEDTPPRLVQLR 453
Db	402 QQILVNHARCPYVRLRSHCRPRTAAHOVAGAL-----NTTSPRLMNLR 447
Qy	454 QHSSPQWVQGYFVACRLRLLPVGGLWGRHNRERRFLRNTKKFISLGKHAKLISLQBLLTWMS 513
Db	448 LISSPQWVYGFQACVGLVPPLGSHHNQRFFPKVTFISLGKDLKLSQBLLTWMS 507
Qy	514 VDCAWLRRSPGCVPAAEHRLREELAKFELHWMMSVYVLLRSFYYTETTFQKNRL 573
Db	508 VODCRWLRRSPGNCVPAAEHRLRTRTFLFWMDAYVVEILRSFYYTETTFQKNRL 567
Qy	574 FPFKRTWSKLQSGIOFHKLWVQRLRESEAETRQHREARPAALTSRTRFISLGKDLRWTWMS 633
Db	568 FPFKRTWSKLQSGIOFHKLWVQRLRESEAETRQHREARPAALTSRTRFISLGKDLRWTWMS 627
Qy	628 YMSY -NGTRAFPKGKQAHFTQCLKLTVFVNLTKHNLGASVGLNDLYRTWTF 686
Db	694 VLRVRAADPPPELYFVYDVTGAYDTIPODRLETEVIASIIK-PONTCVYRVAQKAH 752
Qy	634 VMDYYVGAARTPRREKRAERTSRVKAFLSVNTERARRPGIGASVGLDDIHTRAWTF 693
Db	687 VLRVRLTDPAPRMYFVYDVTGAYDTIPODRLETEVIASIIK-PONTCVYRVAQKAH 746
Qy	753 GIVTRKAFKSHVSLTLDQYMFQVHQL-EITSPLRPIAVLHQSSSNEASSGLFDVFL 810
Db	747 GQIKHKSPPRQVSTLSDLQPHMGOFLKHQDSSTSALANSVIEQSLNSNEASSLDFL 806
Qy	811 RPFMCHHAIRGKSKYVOCQGIPGOSLSTLCLSGYCDMENKLFLAGIRRGDLILRLYVDF 870
Db	807 RPFVNSVVKIGRCYVOCQGIPGOSLSTLCLSGYCDMENKLFAEYQDGLLRLFVDFD 866

CC	or send an email to license@isb-sib.ch).
CC	
DR	AF051911; AAC0933.1; .
DR	AF073311; AAC34821.1; .
DR	AF029235; ABB84200.1; .
DR	MGI; MGI-11202709; Tert; .
DR	InterPro; IPR000417; Rvnse.
DR	InterPro; IPR003515; telomerase_RT.
DR	Pfam; PF0078; Rvt; 1.
DR	PRINTS; PRO1365; TELOMERA8ERT.
KW	DNA-binding; Nuclear protein; Ribonucleoprotein;
KW	RNA-directed DNA polymerase; Telomerase; Transferase.
PT	CONFLICT 553 553 I -> V (in Ref. 3).
SQ	SEQUENCE 1122 AA; 127977 MW; F85266905DD6558C CRC64;
Query Match	58.8%; Score 3505; DB 1; Length 1122;
Best Local Similarity	64.4%; Pred. No. 2-28-210; Gaps 13;
Matches	719; Conservative 122; Mismatches 260; Indels 52;
Db	1 MPRAPRCAVRSLSRSYREVLPATFVRLGPQGWRVLRQGDPAAPFALVAQCLVCPW 60
Qy	1 MTRAPRCPAVRSLSRSYREVLPATFVRLGPQGWRVLRQGDPAAPFALVAQCLVCPW 60
Db	61 DARPPPAAPSFQVSCLKELVARYLQLRCERGAKNVLAFGFAALLDARGCGPPEAFTTSVR 120
Qy	61 GSQPPPADLSFHQVSSLKELVARYLQLRCERGAKNVLAFGFAALLDARGCGPPEAFTTSVR 120
Qy	121 SYLNTNTDALARSGAWGILLRRGGDIDVYHLARCAFLVLPASCATQVCGPLYQGA 180
Db	121 SYLPNTVIELTRVSGAWMILLSSRGDDLVYLHCAFLVLPASCATQVCGPLYQGA 180
Qy	181 ATQARPPPHAS-GPERRLG-----CERAWNESSVREAGVPLGPQPLPAPGARRGSAARS 231
Db	181 TTDIWPSVSAISYRPRVPRVGRNFTNIRELQIKSSSROEAKPLALPSGTKRLSLSSTS 240
Qy	232 LPLPKRPRGAAPEPERTPVQGGSWAHPGRTRGSPDRGFCVSPAR----PAEATTSLE 286
Db	241 VPSAKKARCYPVPRVEEGP-----HRQVLPPTSGKSM--VPSPARSPPEVPTAERDSSK 292
Qy	287 GALGSTRSHPSVGRQHAGGPPSISRPRPWPDTCPVPPYTAETKHFLLYSSGD-KEQLRSF 345
Db	293 GKVSDLSLGSVCKKHKPSSTSLLSPQNAFOLQRFLIETRFLYGRGDQERLNSSP 350
Qy	346 LLSLRPSTGTGARRIVETFLGSRSPWMPGTPRRLPRLPORYWONRPLFILELLGNHAQSPY 405
Db	351 LLSNIPQNLNTGARRIVETFLGSRSPRTSPLCRLTHRILSRRYQWQMPPLQQLVYTHAEQY 410
Qy	406 GVLKTHCPRLRAA--VTPAAGVCAREKPGSVAAPEEEDTDPRRLVQLLRQHSSPQWYVY 462
Db	411 VRLRSHCRRFTANQVTDAL-----NTSPSPHMDLRLRHSSPQWYVY 452
Qy	463 GFWRACLRLRUVPPGIGWGSRHNEREFLRNTKKFFISLGKHAKLSQLQELTMKMSYRDCANWRR 522
Db	453 GFLRACLKCVSASLWGRTHNEREFLRNTKKFFISLGKHAKLSQLQELTMKMSYRDCANWRR 512
Qy	523 SPGVGCPAHEHRREELIANKFLWLMSTYVVELRSFVYVTEFTFQKNRLFFYRKSTWS 582
Db	513 SPGKDRVPAEHRREELIANKFLWLMSTYVVELRSFVYVTEFTFQKNRLFFYRKSTWS 572
Qy	583 KLSQSGIROHLKRVOLRELESEAVERQHREARPAALTSRFLPKDGLRPIVNMDDVYGA 642
Db	573 KLSQSGIROHLKRVOLRELESEAVERQHREARPAALTSRFLPKDGLRPIVNMDDVYGA 632
Qy	643 RTFIREKRAERLTSRKVAFPSVNLAYERARRPGJLGAASVIGLDDIHRARTFVLRVADDP 702
Db	633 RALGRKQAOHFTQRLKLTSMSMLYERTRPHLNGSSVQGMDIYTRTFRVLRVADDP 692
Qy	703 PPELYFVKYDVTGAYDTIPDRLTEVIASTIK-PONTYCYRRAVQKAHGHYRKAKS 761
Db	693 TPRMYFVKYDVTGAYDAPQGKLYEVVANMRHSESTYCTROZAVRDRSDQGVHKSRR 752
Qy	762 HVSTLTDQPYMRCQFVAHQBT--SPRLDAVIVBOSSELINEASGGLFFYFLRMCHHVR 819
Db	753 QVTTLSDIQPYMCGQFLKHLQDSASALRNSVYIEQSISMNESSSSLDFFLHLFRHSVVK 812
Qy	820 TREGKSYVOCQGIPQGSTLSTLJLSCYGDMENTKLFAGTIRRDGLLRLYDDFLVTPHLTH 879
Db	813 IGDRCytcQGIPQGSSLSTLSCFGDMENKLPAEYQDGLLRLFVDDFLVTPHLTH 872
Qy	880 AKTFLRLTLYRGVBYGCYVNLAKTUVNNSPVEDEALGGTAFVQMPAHGLFPWCGSLLLDRT 939
Db	873 AKTFLRLTLYRGVBYGCYVNLAKTUVNNSPVEDEALGGTAFVQMPAHGLFPWCGSLLLDRT 932
Qy	940 LEVQDQSSYARTSIRASLTNFNGKAGRNMRKLFGYURLKCHSLFQDQNSLQTVCT 999
Db	933 LEVFDYDGYAQTSIKTSLTFQSVFKAQKTMNKLSSVLRKCHGLFQDQNSLQTVCT 992
Qy	1000 NIYKILLQOAYRFHACYQLOPFFHQVNKNPFTFLRVISDTASLYCISLKAQKAGMSLGAK 1059
Db	993 NIYKILQOAYRFHACVQLPQRVKNLTFPLGISSQASCYVLLKVNPGMTLKAS 1052
Qy	1060 GAAGPLPSEAQNQVNLCHOAFLKLUTRHRVTTYVPLGLSRTAQTSLSRKLPGTLLTALEAA 1119
Db	1053 GS--FPPEAAHWLYCQFLKLAAHSTYKCLGPRTAQKULCRKLPPEATMTLKAA 1109
Qy	1120 NPALPSDFKTILD 1132
Db	1110 DPALSTDFTQILD 1122
RESULT	7
Q9UBR6	PRELIMINARY;
ID	PRT;
Q9UBR6	524 AA.
AC	Q9UBR6;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE	Telomerase reverse transcriptase (Fragment).
GN	Name=TEXT;
OS	Homo sapiens (Human).
OC	Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]_SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RX	MEDLINE-99144726; PubMed=10022128;
RA	Greeneberg R.A., O'Hagan R.C., Deng H., Xiao Q., Hann S.R., Adams R.R., Lightsteiner S., Chin L., Morin G.B., Depinho R.A.;
RT	"Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation.";
RT	Oncogene 18:1219-1226(1999).
RN	[12]_SEQUENCE FROM N.A.
RP	MEDLINE=99140777; PubMed=9982778;
RA	Wu K.J., Grandori C., Amacker M., Simon-Vermot N., Polack A., Liinger J., Dalla-Favera R.;
RT	"Direct activation of TERT transcription by c-MYC.";
RL	RT Genet. 21:220-224(1999).
RN	[13]_SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RA	Dierest A.-L., Amacker M., Reichenbach P., Nabholz M., Lingner J.;
RL	Submitted (DB-1998) to the EMBL/GenBank/DBJ databases.
RN	[4]_SEQUENCE FROM N.A.
RA	Szutorisz H., Palmquist R., Roos G., Stenling R., Schorderet D., Riedel R., Lingner J., Nabholz M.;
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF119487; ADD34164.1; -
DR	EMBL; AF114847; ADD34164.1; -
DR	GO: GO:0003364; F:RNA-directed DNA polymerase activity; IEA.
KW	RNA-directed DNA polymerase.
FT	NON_TER 524
SQ	SEQUENCE 524 AA; 57932 MW; 5F47DEF01832B1B CRC84;
Query	Match 47.4%; Score 2825; DB 2; Length 524;
Best Local Similarity	100.0%; Pred. No. 2.8e-168;

Matches	524;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;		
Qy	1	M	R	P	R	A	V	R	S	L	R
Db	1	M	R	P	R	A	V	R	S	L	R
Qy	61	D	A	R	P	P	A	P	S	F	R
Db	61	D	A	R	P	P	A	P	S	F	R
Qy	121	S	Y	L	P	N	T	V	D	V	L
Db	121	S	Y	L	P	N	T	V	D	V	L
Qy	181	A	T	Q	A	R	P	P	H	A	S
Db	181	A	T	Q	A	R	P	P	H	A	S
Qy	241	G	A	A	P	E	P	R	T	P	G
Db	241	G	A	A	P	E	P	R	T	P	G
Qy	301	R	Q	H	H	A	G	P	S	T	R
Db	301	R	Q	H	H	A	G	P	S	T	R
Qy	361	V	E	T	F	I	G	S	R	P	N
Db	361	V	E	T	F	I	G	S	R	P	N
Qy	421	P	A	A	G	V	C	A	R	E	K
Db	421	P	A	A	G	V	C	A	R	E	K
Qy	481	R	H	N	E	R	R	L	T	N	K
Db	481	R	H	N	E	R	R	L	T	N	K
RESULT 8											
Q6RDB0	1D	Q6RDB0		PRELIMINARY;		PRT;	1346	AA.			
AC	Q6RDB0;										
DT	05-JUL-2004			(T-EMBLrel. 27, Created)							
DT	05-JUL-2004			(T-EMBLrel. 27, Last sequence update)							
DT	05-JUL-2004			(T-EMBLrel. 27, Last annotation update)							
DE											
GN											
Name-TERT;											
OS											
Gallus gallus											
Metzger, Chordata; Craniata; Vertebrata; Euteleostomi;											
Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;											
OC											
NCBI_TAXID=208526;											
RN	[1]										
SEQUENCE FROM N.A.											
RA											
RL											
Submitted (DBC-2003) to the EMBL/GenBank/DBJ databases.											
EMBL:AY502592; AAS793.1;											
DR											
GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.											
DR											
Interrr: IPR0136545; Telomerase_RT.											
PRINTS: PR01365; TELOMERASE_RT.											
KW											
RNA-directed DNA polymerase.											
SEQUENCE 1.346 AA; 155316 MW; E93A8B64FB64D40 CRC64;											
Query Match											
Best Local Similarity											
Matches 593; Conservative 159; Mismatches 350; Indels 242; Gaps 29;											
9 AVRSLLRHYSREVLPATFVRL - SPQGRFLVQRSQDPA-AFRALVAQCLVCVPMNDARPP 65											
25 AVLGAIRGCAEXTPLAEFVRLQEGTGEVVLQDADACYRTFVSCUVCVPRGARAI 84											
66 PAAPSPFQVSCIKELVRLCERGAKNVLAFGFALLDARGGPPBEATTSVRSYLPN 125											
Db											
Qy	85	P	R	I	C	F	Q	L	S	S	E
Db	126	T	V	D	A	R	G	S	A	T	Q
Qy	145	T	V	E	T	R	I	S	G	I	W
Db	186	P	P	P	P	H	A	S	S	R	Q
Qy	204	P	S	G	F	Y	R	I	S	R	Y
Db	231										
Qy	257	K	R	R	H	R	I	Q	S	L	G
Db	244	P	E	P	T	P	V	G	G	S	W
Db	317	V	E	T	A	R	K	V	I	E	S
Qy	257	A	H	P	R						
Db	374	N	E	M	C	G	P	S	V	Y	H
Qy	265	P	S	D	R	G	F	-C	V	S	P
Db	434	P	N	R	G	E	R	I	R	N	T
Qy	320	P	C	P	P	Y	A	T	R	P	L
Db	485	S	R	S	T	Y	E	K	P	L	Y
Qy	373	P	G	T	R	P	L	P	Q	Y	W
Db	545	P	Q	Q	W	K	R	K	H	T	E
Qy	419	V	T	P	A	G	V	-	-	-	-
Db	605	L	P	G	E	A	K	T	N	S	T
Qy	455	H	S	S	P	N	O	Y	G	V	R
Db	664	H	S	S	H	O	Y	G	F	V	R
Qy	515	R	D	C	A	M	L	R	S	P	R
Db	724	N	D	C	W	M	R	L	A	G	N
Qy	575	F	Y	R	K	S	V	W	S	L	Q
Db	784	Y	Y	R	K	F	W	G	L	Q	N
Qy	635	N	M	D	Y	U	V	G	A	T	F
Db	844	R	L	S	R	V	E	G	Q	L	K
Qy	692	T	F	V	L	R	-	-	-	-	-
Db	1024	F	L	Q	M	H	N	I	L	E	R
Qy	869	D	F	L	L	T	P	H	T	A	K
Db	1084	D	F	L	L	T	P	H	T	A	K
Qy	929	F	W	C	G	I	L	L	T	R	T

Db	1143	SWCGLLUDVQTLLEVYCDYSSYAPTSIISLSFNSSR1AGRNMCKLTLAVLKUCHPLLD 1202	Qy	320	FCPPVYAAETKGFLYSSGDKEQLRPSFLSSLRPSLTGARRLVEETFLGSRPW-----M 372
Qy	989	LOYNSLOTYCTNTYKLLIQAYRFAUQVQLQPFHQWQMKNPTEFLRUISDASLCKYSILK 1048	Db	485	SRSTYFEKFLLTSRSYQYFPFSFLSRLQCGAGGRLIEFTIFLSONPLKEQQNQSL 544
Db	1203	LKINSLQPVLNTYKIFLQAYRFAUQVQLQPFHQWQMKNPTEFLRUISDASLCKYSILK 1262	Qy	373	PGTPRRLPLRPLPQYQMRPLPFLLEGHNHQCPYQVLLKTHCP-----LRAA 418
Qy	1049	AKNAGMSIGAKGAGAAGPLPSEAYQWLCQAPLKLTRHRVTVPLQSSLRATAQTSQSLKP 1108	Db	545	PQQKWKCKLKPQWMLREKCPVLYFLRKNCPVVILSEACLKTKTEFLQAA 604
Db	1263	AKNPGVSLGSKDAGMFFEEAELCQHAFYVQLSNKVKYKCLAKPLKTYKOMHLFKIP 1322	Qy	419	VTPANGV-----CAREKPO-----SVAP-----EDDPFRVYQLRQ 454
Qy	1109	GTTLTAAEANPAPLPSDFKTLID 1132	Db	605	LPGEAKVHKHTGEKESTGTAPSFLAPPSSVLAQGPERGEQHAEQSDP-LIRELRLQ 663
Db	1323	RDTMELLKTVTEPSLCCQDFKTLID 1346	Qy	455	HSSPQVYGFVCLARRLYPPGLWSRHNERRFLRNTKFFISIGKHAKSLSQELTWKNSV 514
RESULT 9					
AAAS75793		PRELIMINARY;	PRT;	1346	AA.
ID	AAS75793;				
AC	AAS75793;				
DT	31-MAR-2004	(TRIMBLrel. 27, Created)			
DT	31-MAR-2004	(TRIMBLrel. 27, Last sequence update)			
DT	31-MAR-2004	(TRIMBLrel. 27, Last annotation update)			
DE		DElomerase reverse transcriptase.			
GN		TERT.			
OS		Gallus gallus gallus.			
OC		Eukarya; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC		Archaeobacteria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC		Gallus; Gallus gallus.			
RN	[1]	NCBI_TAXID:20856;			
RP		SEQUENCE FROM N.A.			
RA		Delany, M. E., Daniels, L. M.			
RL		Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.			
EMBL		AY50592; AAS7793 1;			
RN		RNA-directed DNA polymerase.			
SO		SEQUENCE 1346 AA; 1555186 MW; E93A8B64FB6A4D40 CRC64;			
Query Match					
Best Local Similarity	43.4%	Score 2590; DB 2;	Length 1346;		
Matches	593;	Conservative 159; Mismatches 350; Indels 242; Gaps 29;			
Qy	9	AVRSLLRSHYREVLPLATFVRL-GPQGWRLLVQRGDPA-AFRALVAQCLVCVWDARPP 65	Db	809	FLRFLCHAVRTRGKSYVQCGQIPGSLSLTLICSLCYGDMANLFGIRRQDGLLRLVD 868
Db	25	AVLGLRGCAEXTPFAEYVRLQESGTGEVEVLRGDDAQCYRTFVSCQVVCYPRGAAI 84	Qy	1024	ELQMLHNNTLEIGHRYIQCQSGIPQGSLSLTLICSLCYGDMENKLLEGIQDQGVLILID 1083
Qy	66	PAAPSPRQVSCLKEVAVLQVLRGKVNLAQFSLIDGARGCPEAFTTSYRSPYLN 125	Db	869	DFLFLVTPHILTHAKFLRFLYRGEVPEYGCVUNLRKTVNFPEVEDALGGTAFYQMPAHGLF 928
Db	85	PRPICQQLSSQSEVITRIVYRCLCKKRNLTAGYSLDENSCHFVRLPSSCIVYSN 144	Db	1084	DFLFLVTPHILMQARTFLTRIAAGIPEYGLINAKKTIVNFPV-DDIPGCSKFKHLPDRLI 1142
Qy	126	TYTDAURGSGAWGLLIRRGDVLVHLLARCALFVLPAPSCAYQVCGPPLYOLGAATQAR 185	Qy	929	PWCGLLIDTRTLEYQSDYSSYARTSISTRASLTPNNGKFAGRNMRRKLFGVTLIKCHSFLD 988
Db	145	TVTETIRISLGLWEILSRRIGDVMYLLCFLMVPPENCYQVCGGPOIYEL-ISRNGV 203	Db	1143	SWGGLLUDVQTLLEVYCDYSSYATFTSRSLSNSR1AGKMKCULTAVLKUCHPLLD 1202
Qy	186	PPP-----HAS---GPRRLIGCERAWNHSVREAGVPLGLPAPPARRGGSASR- 230	Qy	989	LQVNSLQTVCTNTYKLLQAYRFAHCVLQBLPHQQWQKNPFFLRLVSDASLCKYSILK 1048
Db	204	FSPGFVRRYRSRFKNSLDDYVRLVFLHR---HYLSSQWVKCRP---RRRGRVSSRR 256	Db	1203	LKINSLQTVLVLNTYKFLQAYRFAHCVLQBLPQKVRNNPDEFLRISDASCYFILK 1262
Qy	231	-----SLFLP-----KPRRRAA 243	Qy	1049	AKNAGMSLGAKGAAGPLPSEAVQWLQHQAFLKLTRHRVTVPLGLSLRATAQTLSRKLP 1108
Db	257	KRRSHRIQSLRSGYQPSAKUNFOAQRIQSTVTALEKQSCSSLCLPARAPSLSKRRDDEQ 316	Db	1263	AKNPGVSLGSKDAGMPEFAEWLYCAYHAFVKLNSHVKVYKCLKPLKVYKMHFLFGKIP 1322
Qy	244	PE-----PERTPYCQG-----SW-----	Qy	1109	GTTLTALEAAANPALPSDFKTLID 1132
Db	317	VEITAKRKVIMEKETBQASIVPD---VNQSSQRHGTWSHYAPRAGLKEHYISRS 373	Db	1323	RDTMELLKTVTEPSLCODFKTLID 1346
Qy	257	-----AHFGR-----TRG-----	Qy	RESULT 10	
Qy	374	NSEMSGPSVYHRSHGPVADKSSFQPGVQGNKRIKTCGAERAENRGIEMYINPKHK 433	Qy	Q9DE32	PRELIMINARY; PRT; 1191 AA.
Db	265	PSDRGF-CVYSPARAE---EATSLLEGALSGTRHSHSVGRHAGPSTSPPRMDT 319	AC	Q9DE32	
Qy	4	PNRGRGIERINPNTKPELNSVQTEPMEGASSGDRKQE-----NPBAHLAKQPLNTL 484	DT	Q9DE32	
Db			DT	01-MAR-2001 (TRIMBLrel. 16, Created)	
			DT	01-MAR-2001 (TRIMBLrel. 16, Last sequence update)	
			DT	01-OCT-2003 (TRIMBLrel. 25, Last annotation update)	
			DE	Telomerase reverse transcriptase.	
			GN	Name=TERT;	
			OS	Xenopus laevis (African clawed frog).	
			OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			OC	Amphibia; Batrachia; Anura; Mesobatrachia; Bipoidea; Pipidae;	

OC	Xenopodinae; Xenopus	
NCBI_TaxID	8355;	
OX		
RN		
RP		
RX	SEQUENCE FROM N.A. ; PubMed=11602347; MEDLINE=21488334; PubMed=11602347; RX	
RA	Kuramoto M., Ohsumi K., Kishimoto T., Ishikawa F.; "Identification and analyses of the Xenopus TERT gene that encodes the catalytic subunit of telomerase." ;	
RT	Gene 277:101-110(2001); EMBL: AF212299; AAGT3537..1; -	
DR	GO: 0005634; C:nucleus; IEA. DR	
DR	GO: 0010377; F:DNA binding; IEA. DR	
DR	GO: 0003723; F:RNA binding; IEA. DR	
DR	GO: 0003964; F:RNA-directed DNA polymerase activity; IEA. DR	
DR	GO: 0003721; F:telomeric template RNA reverse transcriptas. . ; IEA. DR	
DR	GO: 0016740; F:telomerase activity; IEA. DR	
DR	GO: 0006278; P:RNA-dependent DNA replication; IEA. DR	
DR	InterPro: IPR00477; RVT; InterPro; IPR003545; Telomerase_RT. DR	
PFam:	PF00078; RVT; 2; PRINTS; PRO1365; TELOMERASERT. KW	
RNA-directed DNA Polymerase; Transferase. SEQUENCE 1191 AA; 138016 MW; 9BD9776869A57D6 CRC64;		
Query Match	38.9%; Score 2316.5; DB 2; Length 1191;	
Best Local Similarity	42.4%; Pred. No. 4 9e-136;	
Matches	518; Conservative 201; Mismatches 381; Indels 123; Gaps 25;	
Db	1 MPRAPRCAVRSTLRSRYREVLPPLATFVRLG-POGWR--LVQRGDPAAFRALVAQCLVC 57	
Db	1 MPRATGGATLSTLQLRQLGIVETDYLQPGGIKVPLJEGSDSKFRSFRVAELVVC 60	
Qy	58 VPWDARPPPAAPSPFQVOSCLKEVAVLQLCERGAXKVLAFGALLDARGGPPEATT 117	
Qy	61 IPRGTKPLKPLSPVSPFLSTOREVAVTQRCIECKKRXNVLAFLGYLVD-EKNSLNTRTP 119	
Qy	118 SRSYLPNTVTDALRGSGAWLGLLRLRGGDVLVHLLARCAFYLVAPSCAYQVCGPFLY- 176	
Qy	120 NICYNFPNPTTTTISTSILWETLILTRVDDVMWLEQSCISYFVPPRCYQITGQPYT 179	
Qy	177 -----QLGAAATOAR-----PPPHASGPRRRLGCEAWNHSYRE 209	
Db	180 LPDDDFVLFQSQFTQSNTVNLRLYTKRNVFHRLRKYKLKHSMTSRM-----LTWRRNRS 234	
Qy	210 AGYPLGLPAPGARRGGSARSRL-----PLPKPGRPRGAPE-----PRPTPGQ 254	
Db	235 SGILIRSKTSMAVTTIEHSKRKLCUKSKDTCIVIPDKRDNLDKDDTVHDFLPMCRSISYL 294	
Qy	255 SWAHPGR-----TRG-PSDRGFCVVSPPARAEATSLLEGALSGTPH----- 294	
Db	295 SAMYPTKTNQVQTGLTSGYKTKTFQOKPVSEQKTTAFTYSGADONLSKDNVNKL 354	
Qy	295 SHPSVGROHAGGPSTSRPRPMDTPCPVVAETKHFY-SSSDKEQURPSFLSSLRPS 353	
Db	355 'TNAV-----LSEFNIFIDFGRFTYLISYKKGFSSEPSLNSLSDT 401	
Qy	354 LIGCARRLVETIPIGS-----RPMRPGTPRPLPRLQYRQWMPRLPLELQGNAQCQY 405	
Db	402 PSQSQKLVETIIFLSNFLAEQNFIQPKRDENCRCY--KLPKRYWMKPHQELQNHKKEPY 459	
Qy	406 GVLKTHCPRLPRAATPAAGCVAEKPQGSSVAABEED-----TDRRLYVLLRQHSS 457	
Db	460 LYVLNKHCVPRSSM---ACSEKR--SLQKNRIEENDGKQKHTTKKANLLSLKQHSS 511	
Qy	458 PHOYYGFVYRACLRLVPPGLGSRHNERFLRNTKFKFSL-GKHAKLSQLTWTMVSVD 516	
Db	512 IWDYMFRECLNNVPD1MGWSHNNKCRFRNVSFLSFQGKFLSLSLWMSMR/ED 571	
Qy	517 CAWLRRSQGVGCVPAEAHRLREETLAKFLHMLMSVYVYLRLRSPFVYETETFQKNRLLPY 576	
Db	572 CSWIRLQKSDHFVPASEHLLREKILAKFVWLMDTYVQLKLSFFYVETMFQKHLRLFY 631	
Qy	577 RKSVWLSQISIGTRQLRQVREARPLTLRSLRFLPKPDGSRPBYN 636	
Db	632 RKSTWKLQNLQNLGKHLKELYKLRSLUSISDELENMQKVNPLVSLRFLPKTNGLRLRISKI 691	
Qy	637 DYYVGCARTER--REKRAERLTTSVRLAFLSVYARRPGLGASTGLDDTHRAWRTFV 694	
Db	692 SSTLSSQQSTENQERKHHFSSQIRNLFSVLYENRNCNSLIGSSFGMDDLYKWRKRFV 751	
Qy	695 LRV-RAQDPPEPELYFVKDVTGAYDTIPQDRLTTEVASYI1KP--QNTYCVRYAVVQKAA 751	
Db	752 LDFERKPVQEVLQFVKTQDVGATDIPHSKLDDEVTSKVINPNAFVYCYRRATYTSVDP 811	
Qy	752 HGHVRKAFKSHVSTLTDLQPMYPOVPAHLOETSPDRAVIEQSSSLNEASGLFVFLR 811	
Db	812 TGRTRIKSEKRVHSELAADVLPNMKQFVSNQEQEKNLRLNTLVEQNLINNESSVKLAVFQQ 871	
Qy	812 FMCHHAVRTRGKSYVQCOGIGPOGISTLTLCSLYCGMDMENLFGAGTRDGHLLRLVYDDFL 871	
Db	872 FIRSHLRLKDRYTMQCCGPGQSMHATLISLCLGDMENALGGIQRNGYLMRLDDFL 931	
Qy	872 LYTPHILTHAKTFLRLTVREYPEYEGCVNLRLKTVNFPYED--EALGGTAFYOMPAGLFP 929	
Db	932 LYTPHLDQAKTFLRLTAEGIPLQYQGSISPORTVNPVDDIPEC--SEVOLPSCLFR 988	
Qy	930 WCGLLLDTTLEVQSDYSSSTARTS*TRANSIPLFNRGKAGRMRKLELGULRJKCSFLDL 989	
Db	989 WCGLLLDTQLDVYDYYSSACTSIRSSMTFCHSSAAGKVMQKULURLJKCSFLDL 1048	
Qy	990 QVNSELQTVCTNIYKILLQOAYRFHACVLQPLFHQQWKNPTEFLRVTSDASLCYSLKA 1049	
Db	1049 KVNSLRTVCINTYKILLQOAYRFHACVQLQPLFQQRVMNPPFFLTISDAPCYTTFKA 1108	
Qy	1050 KNAGMSLGAKGAAGLPLSEAVQWLNQHQAFLKLRLRHTVYVPLLSLRTAQTSRSLKLPG 1109	
Db	1109 KKNKDTRGKVDVSOCNFNEAVQWLNQYQAFLTKLNHNVKLYXCLGDLQNCRMQLSRLSQ 1168	
Qy	1110 TTIALEAANPALSDFPTILD 1132	
Db	1169 DTIELUKSVDSSLHKDFSCIMD 1191	
RESULT 11		
Qy	094807 PRELIMINARY; PRT; 523 AA.	
Db	094807 ID 094807 PRELIMINARY; PRT; 523 AA.	
Qy	094807_1 AC 094807_1 PRELIMINARY; PRT; 523 AA.	
Db	094807_1 DT 01-MAY-1999 (TREMBLrel. 10, Created)	
Qy	094807_1 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)	
Db	094807_1 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
Qy	094807_1 DE Telomerase transcriptase (Fragment).	
Db	094807_1 DE Name=hTERT; Homo sapiens (Human).	
Qy	094807_1 OS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	
Db	094807_1 OC NCBI_TaxID=9606;	
Qy	094807_1 RN SEQUENCE FROM N.A.	
Db	094807_1 RP MEDLINE=99137484; PubMed=9973199; Takakura M., Kyo S., Kanaya T., Hirano H., Takeda J., Yutbudo M., Inoue M.; "Cloning of human telomerase catalytic subunit (hTERT) gene promoter and identification of proximal core promoter sequences essential for transcriptional activation in immortalized and cancer cells.".	
Qy	094807_1 RX EMBL; AB016767; BA747247; -.	
Db	094807_1 FT NON TER 523 523	
Qy	094807_1 SQ SEQUENCE 523 AA; MW: 86DB562DDECC93DA CRC64;	
Db	094807_1 Query Match 37.0%; Score 2207.5; DB 2; Length 523; Best Local Similarity 78.7%; Pred. No. 1..1e-129; Matches 435; Conservative 3; Mismatches 56; Indels 59; Gaps 6;	
Qy	1 MPRAPRCAVRSLRSHYREVPLATFVRLGPOQRLYORGDPAAFRALVAQCLYCVPW 60 1 MPRAPRCAVRSLRSHYREVPLATFVRLGPOQRLYORGDPAAFRALVAQCLYCVPW 60 1 MPRAPRCAVRSLRSHYREVPLATFVRLGPOQRLYORGDPAAFRALVAQCLYCVPW 60	

DR	PRINTS; PRO1365; TELOMERASET.
KW	RNA-directed DNA polymerase; Transferase.
FT	NON TER
SQ	1 SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;
Qy	Query Match 33.8%; Score 2016; DB 2; Length 575;
Db	Best Local Similarity 67.6%; Pred. No. 1.2e-117;
Qy	Matches 391; Conservative 71; Mismatches 110; Indels 6; Gaps 3;
Db	1 RSFPYTTETFQKNRLFFYRKTSWKLQSGIGIROLHKLKVQLRELSAEVYQHREARPALL 617
Qy	558 RSFPYTTETFQKNRLFFYRKTSWKLQSGIGIROLHKLKVQLRELSAEVYQHREARPALL 617
Db	1 RSFPYTTETFQKNRLFFYRKTSWKLQSGIGIROLHKLKVQLRELSAEVYQHREARPALL 60
Qy	568 TSRLRFIPKPDGLRPIVNNDDYVYGGARTPFREKKAERLTSRKVAKLFSVLYERARRPGLLG 677
Db	1 ICRLRFIPKNGRPIVNNNSMTRALGRKQAHFTORLTKTFSMLVYERTRPHLMLG 120
Qy	618 TSRLRFIPKPDGLRPIVNNDDYVYGGARTPFREKKAERLTSRKVAKLFSVLYERARRPGLLG 677
Db	61 ICRLRFIPKNGRPIVNNNSMTRALGRKQAHFTORLTKTFSMLVYERTRPHLMLG 120
Qy	658 ASVLGDDIHRMARTTEVLVRADDPPELYKVDTGAYDTIQQRLTEVIASTIK-PQ 736
Db	121 SSVLMNDYIYTRWAFRLVRALDQTPTMRYFVKADVTGAYDAIPOQKLVEVVAANVIRHSE 180
Qy	698 ASVLGDDIHRMARTTEVLVRADDPPELYKVDTGAYDTIQQRLTEVIASTIK-PQ 736
Db	121 SSVLMNDYIYTRWAFRLVRALDQTPTMRYFVKADVTGAYDAIPOQKLVEVVAANVIRHSE 180
Qy	737 NTYCVRVAVQVQKAAGHIVRKAFKSHVSTLTDQPYMROFVHILQET--SPLRDAAVIEQ 794
Db	181 STYCIRQAVAVRDRDSCQGHFKHQDSDASALRNSVVIQE 240
Qy	775 SSSLNEASSGLFDVLFRLMCHHAVRIRGKSYVOCQGIPGSLISLTSLCSLICYGDMENKLFLP 854
Db	241 SISNNNESSSLFDFLFLHPSLSSLRDILTGARRL 360
Qy	815 AGIRRGGILLRLVUDFLLUTPLTHAKRFLRLVGRGPPYQGCVUNLRKTVNPEDEAL 914
Db	301 AEYORDGILLRFYDDFLVTPHLDQAKTFLSTLVHGPVPGTTL 360
Qy	855 GGTAFQVNPAGHLEPWCGHLLDPTRLTEVQSDYSSYARTSIRASLTENRFGKAGRMMRKL 974
Db	361 GGARYQDPAHCFPWCGHLLDQTLTEVCDYKGSYQTSIKTSITFQSFKAGTMNKL 420
Qy	895 FGYILRKCHSLFELDLQNSLQTCTVNTIYKILLQAYRFHACVQLPQHQVQWNPKTFFLR 1034
Db	421 LSYTLRKCHGLFELDLQNSLQTCTVNTIYKILLQAYRFHACVQLPQHQVQWNPKTFFLR 480
Qy	935 VIQSTDASLCKSILKAKNGMSLQAKGAGPLPSEAVWQVQHQAFLKLTRHRVTVYVPLLG 1094
Db	481 TISSQASCCYAILVKVNGMTLKAAGS---FPPEFAAHNVCYQAFLKLAAHSVTVYKCLLG 537
Qy	975 SURTAQTOLSRKLPGTGTLLTALEAAANPALSDFXTLID 1132
Db	538 PLTAAQKLCKRPUPEATMILKAADPALSTDQFTILD 575
RESULT 13	SEQUENCE FROM N.A.
QSR266	PRELIMINARY;
ID	O9R266
AC	O9R266;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Telomerase reverse transcriptase (Fragment).
GN	Name=Text;
OS	Mus musculus (Mouse).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON	[1]
RN	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22860253; PubMed=13679242;
RA	Wong S.C., Ong L.L., Er C.P., Gao S., Yu H., So J.B.;
RA	"Cloning of rat telomerase catalytic subunit functional domains, reconstitution of telomerase activity and enzymatic profile of pig and chicken tissues";
RA	Life Sci. 73:2749-2760 (2003).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Wong S., Gao S., Xu X., Yu H.;
RA	"Cloning of rat telomerase catalytic subunit functional domains, reconstitution of telomerase activity and enzymatic profile of pig and chicken tissues";
RA	Life Sci. 73:2749-2760 (2003).
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Wong S.C., Ong L.L., Er C.P., Gao S., Yu H., So J.B.;
RA	"Cloning of rat telomerase catalytic subunit functional domains, reconstitution of telomerase activity and enzymatic profile of pig and chicken tissues";
RA	Life Sci. 73:2749-2760 (2003).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Wong S., Gao S., Xu X., Yu H.;
RA	"Cloning of rat telomerase catalytic subunit functional domains, reconstitution of telomerase activity and enzymatic profile of pig and chicken tissues";
RA	Life Sci. 73:2749-2760 (2003).
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=99144726; PubMed=10022128;
RA	Greenberg R.A., O'Hagan R.C., Deng H., Xiao Q., Hann S.R., Adams R.R.,
RA	Lichtsteiner S., Chin L., Morin G.B., Depinho R.A.;
RA	"Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation.";
RA	Oncogene 18:1219-1226 (1999).
RL	[1]
DR	EMBL; AF121974;
DR	DR GO; GO:003964; F:RNA-directed DNA polymerase activity; IEA.
DR	GO; GO:003721; F:telomeric template RNA reverse transcriptas. . . ; IEA.
DR	GO; GO:0016740; F:transferase activity; IEA.
DR	GO; GO:0002728; F:RNA-dependent DNA replication; IEA.
DR	InterPro; IPR000477; RVTse.
DR	InterPro; IPR000477; RVTse.
DR	Pfam; PF000778; RVT.
DR	Pfam; PF000778; RVT.

RW	RNA-directed DNA polymerase.	
FT	NON TRR 514 514	
SEQUENCE	514 AA: 58382 MW: 3096599776D9BBFD CRC64;	
Query Match	23.0%; Score 1373; DB 2; Length 514;	
Best Local Similarity	56.1%; Pred. No. 1.7e-77;	
Matches	304; Conservative 50; Mismatches 142; Indels 46; Gaps 10;	
Qy	1 MPRAPRCAVRSLRSHYREVPLATVRRGLPQGMWLLVQRCDAFARALVAQCLVCVPW 60	DR GO: 0003677; F:DNA binding; IEA.
Db	1 MTRAPRCAVRSLRSHYREVPLATVRRGLPQGMWLLVQCLVCMHW 60	DR GO: 0003723; F:RNA binding; IEA.
Qy	61 DARPPAPSPFQVSCRELAVRLQLCERAKVIAFGPALLDARGGPPEAFTTSVR 120	DR GO: 0003964; F:RNA-directed DNA polymerase activity; IEA.
Db	61 GSQQPPADLSPHQVQSSKELARVQQLCERNERNVIAFGPELLNARGGPPMAFTTSVR 120	DR GO: 0003721; F:telomerase activity; IEA.
Qy	121 SYLPNTVTDALRGSGAWGLLJRRVGDVDYLHLLARCAFLVYAPSCAYQVGPPLYQLGA 180	DR GO: 0003722; F:transfere activity; IEA.
Db	121 SYLPNTVTDALRGSGAWGLLJRRVGDVDYLHLLARCAFLVYAPSCAYQVGPPLYQLGA 180	DR GO: 0016740; F:RNA-dependent DNA replication; IEA.
Qy	181 ATQARPPHAS_GPRRLG-----CERAMNHSSYRBEAGYPLGLDAGGARRGGSASRS 231	DR InterPro: IPR00215; Prot_inh_serpin.
Db	181 TTDIWPSSVASYRPTREVGFRNFTNLRLQQIKSSQEAQPKPLAPSRGTPKRLSITSTS 240	DR InterPro: IPR00477; RTTse.
Qy	232 LPLPKRPRRGAPEPRTTPVCGSWAHPGRTRGPSPDRGFCTVSPAR-----PAEATSSL 286	DR InterPro: IPR003545; Telomerase_RT.
Db	241 VESAKKARCKCYPVPRVEGP-----HRQVLPPTSGKSW-----VPSAPSPPEVPTAEKDLSK 292	DR InterPro: IPR003545; Telomerase_RT.
Qy	287 GALSGTPTSHPSVGRQHAGGPPSTSRRPRPMDTPCPVPPVAYTKHFLYSSGD-KEQLRPSF 345	DR PRINTS: PRO1365; TELOMERASERT.
Db	293 GKVSDLIS-GSVCCKRKPSSTSLLSPRQNAFOLP-FIETHFLYSSRGDQERLNPSF 350	DR PROSITE: PS00284; SERPIN; UNKNOWN_1.
Qy	346 LLLSLRSPLTGARRLVTETIFGSRPWPMPGTPPRLPUPQRYWQMRPLFELIGLNAQCPY 405	DR RNA-directed DNA polymerase; Transferase; RNA-directed DNA replication.
Db	351 LISNLQFNLTGARRLVEIIFGSRPRTSGPLCRTHLSSRYWQMRPLFQQLVNHAEQY 410	DR RNA-directed DNA polymerase; Transferase; RNA-directed DNA replication.
Qy	406 GVLILKTHCPLRAA---VTPAACGVCAKEPKQGSVAAPEEEDTPRRLVQLRQHSSPQVY 462	DR RNA-directed DNA polymerase; Transferase; RNA-directed DNA replication.
Db	411 VRLRSHCRTFTANQQTDL-----NTSPSPHMDLRLHSSPW 452	DR RNA-directed DNA polymerase; Transferase; RNA-directed DNA replication.
Qy	463 GFVRACTTLLYPPGLMGSRHNERRFLRNTKKFISLQKTHA1SLQELTWKMSVRDCAWLR 522	DR RNA-directed DNA polymerase; Transferase; RNA-directed DNA replication.
Db	453 GFLRACLCKVYASASLNGTRENERRFFNLLKKFISLQKGLSLQELMWKQVMDCHWLRS 512	DR RNA-directed DNA polymerase; Transferase; RNA-directed DNA replication.
Qy	523 SP 524	DR RNA-directed DNA polymerase; Transferase; RNA-directed DNA replication.
Db	513 SP 514	DR RNA-directed DNA polymerase; Transferase; RNA-directed DNA replication.
RESULT 14		
Q9SE99	PRELIMINARY; PRT; 1123 AA.	
ID	Q9SE99; AC: 09SE99;	
DT	01-MAY-2000 (T-EMBL; 1.3, Created)	
DT	01-MAY-2000 (T-EMBL; 1.3, Last sequence update)	
DT	01-MAR-2004 (T-EMBL; 2.6, Last annotation update)	
DB	Telomerase reverse transcriptase catalytic subunit.	
GN	Arabidopsis thaliana (Mouse-ear cress).	
OS	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
CC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;	
CC	euroids II; Brassicales; Brassicaceae; Arabidopsis.	
OX	NCBI_TAXID:3702;	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Landsberg erecta;	
RC	MEDLINE=20079565; PubMed=10611295;	
RX	Fitzgerald M.S., Riba K., Gao F., Ren S.,r. McKnight T.D., Shippen D.E.,	
RA	"Disruption of the telomerase catalytic subunit gene from Arabidopsis inactivates telomerase and leads to a slow loss of telomeric DNA.";	
RT	Proc. Natl. Acad. Sci. U.S.A. 96:14813-14818(1999).	
DR	EMBL; AF1/20297; AAB54276.1; -;	
DR	GO: 0005634; C:nucleus; IEA.	

Db	687	FVVADVEKAEDSVDOGKLLHVIQSFLKDE-YIINRCCRLLVCCGKRSNWNKILVSSDKNS	744	DR InterPro; IPR003545; Telomerase_RT.
Qy	762	HVSTLTLDQPMQFVAHQLOETSPRLRDAYVIEQSSSLNEAASSGLFDVFLREMCHHAIR	821	DR PFM; PF00078; RVT; 1.
Db	745	NFSRFTSTVYNA----LQ-----SIVDKGBBNHVRKDDLMWGNMNLQNLQD	792	DR PRINTS; PRO1365; TELOMERASERT.
Qy	822	GKSYVQCGIPQGSTLSTLCSLCYGMENKLFGI-----RRDGL----	862	DR PROSITE; PS01284; SERPIN; UNKNOWN_1.
Db	793	KSFVYQAGPQHRSLLCFCYGHRLTLYPEELFEEASKDVSKECSREPEELIPTS	852	DR RNA-directed DNA polymerase activity; IEA.
Qy	863	--LQLRVDDEFLVTPHHLHARTFRTLRVGRPEYGCVWNLRKTVNFPEDE-----	912	DR GO:0003677; C:nucleus; IEA.
Db	853	YKLRFIDDLFLVFTSRSQDASSFYHLRGPKDYNCFNETKFINFDKEEHRCSNSRM	912	DR GO:0003723; F:DNA binding; IEA.
Qy	913	--AUGGTAFYOMPAHGLFPNCGLLDTTLETCYDSSYARTSTRASLTENRGFKAGNN	970	DR GO:0003677; F:DNA binding; IEA.
Db	913	FVGDNQGPFR-----WTGLJINSRTEVQDYDTRTSLSGHSSTSVAVONKPVNL	964	DR GO:0003677; F:DNA binding; IEA.
Qy	971	RRKLFGVLRKCHSFLDQVNSLQTCVNLYKILLQAYRFHACVQLQLPFHQQWIK-NP	1029	DR GO:0003677; F:DNA binding; IEA.
Db	965	RQKLCYFLVPKCPLFDSINSEGRINVNLYQFLLAMKFCYVYV--SRFWKHLF	1021	DR GO:0003677; F:DNA binding; IEA.
Qy	1030	TFLERVISDFTASLCVSLIKARNAGMSLAGK-GAAGPLPPEAVOWLCHQAFPLKLTTRHVT	1088	DR GO:0003677; F:DNA binding; IEA.
Db	1022	QTLFKFTITSVYRMLINRVRRTNTGSSFRPVLKLYKEEVILGLDAYIQVLIKNSR	1081	DR GO:0003677; F:DNA binding; IEA.
Qy	1089	YVPLIGSLRTA-----OTOLSKRKLPGTT	1111	DR GO:0003677; F:DNA binding; IEA.
Db	1082	YRMDDIYLKSAKSRSLSQOSSLSELYAT	1110	DR GO:0003677; F:DNA binding; IEA.
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RESULT 15				
Q9SPU7	PRELIMINARY;	PRT;	1123 AA.	DR GO:0003677; F:DNA binding; IEA.
AC	Q9SPU7;			DR GO:0003677; F:DNA binding; IEA.
DT	01-MAY-2000	(TREMBLrel. 13, Created)		DR GO:0003677; F:DNA binding; IEA.
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		DR GO:0003677; F:DNA binding; IEA.
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		DR GO:0003677; F:DNA binding; IEA.
DE		Telomerase reverse transcriptase		DR GO:0003677; F:DNA binding; IEA.
GN	Name=AttERT; Synonyms=FEEL1_190;			DR GO:0003677; F:DNA binding; IEA.
OS	Arabidopsis thaliana (Mouse-ear cress)			DR GO:0003677; F:DNA binding; IEA.
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			DR GO:0003677; F:DNA binding; IEA.
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			DR GO:0003677; F:DNA binding; IEA.
OC	euroids II; Brassicales; Brassicaceae; Arabidopsis.			DR GO:0003677; F:DNA binding; IEA.
OX	NCBI TaxID=3702;			DR GO:0003677; F:DNA binding; IEA.
RN	SEQUENCE FROM N.A.			DR GO:0003677; F:DNA binding; IEA.
RX	SEQUENCE ID=9402974; PubMed=10471830;			DR GO:0003677; F:DNA binding; IEA.
RX	Oguchi K, Liu H., Tamura K., Takahashi H.;			DR GO:0003677; F:DNA binding; IEA.
RA	"Molecular cloning and characterization of AttERT, a telomerase			DR GO:0003677; F:DNA binding; IEA.
RT	reverse transcriptase homolog in Arabidopsis thaliana.";			DR GO:0003677; F:DNA binding; IEA.
RL	FEBS Lett. 457:465-469(1999).			DR GO:0003677; F:DNA binding; IEA.
RN	SEQUENCE FROM N.A.			DR GO:0003677; F:DNA binding; IEA.
RX	EU Arabidopsis sequencing project; EMBL/GenBank/DBJ databases.			DR GO:0003677; F:DNA binding; IEA.
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.			DR GO:0003677; F:DNA binding; IEA.
EMBL	[3]			DR GO:0003677; F:DNA binding; IEA.
EMBL	PIR: T51517; T51517.			DR GO:0003677; F:DNA binding; IEA.
DR	GO: GO:0005631; C:nucleus; IEA.			DR GO:0003677; F:DNA binding; IEA.
DR	GO: GO:0003677; F:DNA binding; IEA.			DR GO:0003677; F:DNA binding; IEA.
DR	GO: GO:0003723; F:DNA binding; IEA.			DR GO:0003677; F:DNA binding; IEA.
DR	GO: GO:003964; F:RNA-directed DNA polymerase activity; IEA.			DR GO:0003677; F:DNA binding; IEA.
DR	GO: GO:0003721; F:Telomeric template RNA reverse transcriptas...			DR GO:0003677; F:DNA binding; IEA.
DR	IEA.			DR GO:0003677; F:DNA binding; IEA.
DR	InterPro; IPR00215; Prot_inh_serpin.			DR InterPro; IPR00477; RVTse.
DR	InterPro; IPR000477; RVTse.			

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Db 793 KSFYVQIAGTPOGHRLSSLCCFYGHHLERTLIPFLEASKDVSSKESREEELIPTs 852
Qy 863 -LLRLVDDFLVTPHHTHAKTFLRLTRGVGPEYGVNLRKTVNNFPEDE----- 912
Db 853 YKLLRPTDDYLFVSTSRDQASSFYRLKHGFKDYNCFMNETKFCINDEKEHRCSSNRM 912
Qy 913 --ALGGTAFYQMPAHGIFPNCGLLIDTRTLEQSDYSYARTSSTRASLTFNRGFAGRM 970
Db 913 FVGDNQEVPFYR-----WTGLLNSRTFEEQDVDTYRLSGHISTFSVAVQNKPVNL 964
Qy 971 RRKLFGVTLRKCHSLFDLQVNSLQTVCTNYKILLQAYRFACTVLQLPFHQQWIK-NP 1029
Db 965 RQKLCYFLVPCPCHPLFDSNINSGETVRNLTYQIFLAAAMKFHCYVVEV--SREWKCHP 1021
Qy 1030 TFFLRVTSIDASLCYSILAKKAGNSLGAK-GAAGPLPSEAVQWILCHQATFLKUTRHVT 1088
Db 1022 QTLFRKPTISYRMPRLINRVRVINTGSSFRPVLKLYKEEVINLGLDAYIQVLLKKNSR 1081
Qy 1089 YVPLIGSLRATAQO--LSRKLPGTTLTALAAAANPAl 1123
Db 1082 YRMLLTLKSAKHSLSQQUSSELYATDERSNSSL 1118

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Search completed: January 10, 2005, 17:38:35  
 Job time : 222 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:32:00 ; Search time 42 Seconds  
(without alignments)  
1787.428 Million cell updates/sec

Title: US-10-053-758-225  
Perfect score: 5961  
Sequence: 1 MPRAPCRAVRSILRSHYRE.....TALEAAANPALPSDFKTLID 1132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.Dep:  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.Dep:  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.Dep:  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.Dep:  
5: /cgn2\_6/prodata/1/iaa/PCMB.Dep:  
6: /cgn2\_6/prodata/1/iaa/backfile1.Dep:  
\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	5961	100.0	1132	3	US-08-851-843A-225	Sequence 225, App
2	5961	100.0	1132	3	US-08-974-549A-2	Sequence 2, Appli
3	5961	100.0	1132	3	US-08-054-030-225	Sequence 225, App
4	5961	100.0	1132	3	US-09-430-023-225	Sequence 225, App
5	5961	100.0	1132	3	US-09-128-054-2	Sequence 2, Appli
6	5961	100.0	1132	4	US-09-321-060-2	Sequence 2, Appli
7	5961	100.0	1132	4	US-09-052-919-2	Sequence 2, Appli
8	5961	100.0	1132	4	US-08-12-911-2	Sequence 2, Appli
9	5961	100.0	1132	4	US-09-040-181B-2	Sequence 2, Appli
10	5961	100.0	1132	4	US-09-721-456-2	Sequence 2, Appli
11	5961	100.0	1132	4	US-09-053-052-2	Sequence 2, Appli
12	5961	100.0	1132	4	US-09-160-3	Sequence 3, Appli
13	5961	100.0	1154	4	US-08-974-549A-613	Sequence 613, App
14	5961	100.0	1154	4	US-08-01-951-323	Sequence 323, App
15	5961	100.0	1154	4	US-09-102-181B-611	Sequence 611, App
16	5961	100.0	1154	4	US-09-717-056-077	Sequence 611, App
17	5961	100.0	1189	3	US-08-974-549A-613	Sequence 613, App
18	5961	100.0	1189	4	US-08-112-951-325	Sequence 325, App
19	5961	100.0	1189	4	US-09-402-181B-613	Sequence 613, App
20	5961	100.0	1189	4	US-09-721-456-613	Sequence 613, App
21	5961	100.0	1200	4	US-08-08-74-549A-612	Sequence 612, App
22	5961	100.0	1200	4	US-08-912-951-324	Sequence 324, App
23	5961	100.0	1200	4	US-09-012-181B-612	Sequence 612, App
24	5961	100.0	1200	4	US-09-121-456-612	Sequence 612, App
25	5961	100.0	1285	4	US-08-974-549A-600	Sequence 600, App
26	5961	100.0	1285	4	US-08-112-951-314	Sequence 314, App
27	5961	100.0	1285	4	US-09-402-181B-600	Sequence 600, App

## ALIGNMENTS

RESULT 1  
US-08-851-843A-225

; Sequence 225, Application US/08851843A  
; Patent No. 6093809

## GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6093809el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.10.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851-843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 0  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 0  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 0  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 015389-002930US  
REFERENCE/DOCKET NUMBER: 36,429  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 225:

330/123  
08/676,967

SEQUENCE CHARACTERISTICS:

LENGTH: 1132 amino acid

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-851-843A-225

Query Match 100.0%; Score 5961; DB 3; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MPRAPCRAYRSLLRSHYREVPLATEFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCYBVW 60

1 MPRADRCRAVSLRSLLRSHYREVPLATEFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCYBVW 60

61 DARPPAAPSFRQVSCLKEELVARVQLQRCERGAKVNLQAGFALLDQAGCPAAFTTYSR 120

61 DARPPAAPSFRQVSCLKEELVARVQLQRCERGAKVNLQAGFALLDQAGCPAAFTTYSR 120

121 SYLPNTVTDALRGSAWGLLRLRVDDVHLARCAFLVLPSCAVQVCGPPLYQJGA 180

121 SYLPNTVTDALRGSAWGLLRLRVDDVHLARCAFLVLPSCAVQVCGPPLYQJGA 180

181 ATQARPPPHASGPRRLGCRARNNSVREAGVPLGLPAGARRGGASRSRSLPJKRPRR 240

181 ATQARPPPHASGPRRLGCRARNNSVREAGVPLGLPAGARRGGASRSRSLPJKRPRR 240

241 GAAPEPERTVYQGCSWAHPTRTEPSDRGFCVYSPARABEATSLLEGALSHTHSPYVG 300

241 GAAPEPERTVQGCSWAHPTRTEPSDRGFCVYSPARABEATSLLEGALSHTHSPYVG 300

301 RQHAGPSTSRRPRPWDPFCPPVYATRHFPLYSSQDKEQLRSFILLSLRPLTGARL 360

301 RQHAGPSTSRRPRPWDPFCPPVYATRHFPLYSSQDKEQLRSFILLSLRPLTGARL 360

361 VETIFLGSRWMMPGTPRLPRLPRYQWNRPLFUELLGNAHQCPYGVILKTHCPLRAVT 420

361 VETIFLGSRWMMPGTPRLPRLPRYQWNRPLFUELLGNAHQCPYGVILKTHCPLRAVT 420

421 PAAGYCAREPKPQGSAVAAPEEDEDTIPRLVQLLRHSSPMQVYCFVRACLRLVPPGIGWS 480

421 PAAGYCAREPKPQGSAVAAPEEDEDTIPRLVQLLRHSSPMQVYCFVRACLRLVPPGIGWS 480

481 RHNERFLRNTKKFISLGKAHLSLQELTWKMSYRDCAMLRRSPGVGVCPAAFHRLREI 540

481 RHNERFLRNTKKFISLGKAHLSLQELTWKMSYRDCAMLRRSPGVGVCPAAFHRLREI 540

541 LAKFHLWLMSVVYELLSPFYYETTFQNRNLFYRKSVWSKLQSIGTRQHLKRVQRE 600

541 LAKFHLWLMSVVYELLSPFYYETTFQNRNLFYRKSVWSKLQSIGTRQHLKRVQRE 600

601 LSEAEVRQREARPALLSLRFPKPGDHLRPTYNNMDVYVGARTFRERKAELTSRKYA 660

601 LSEAEVRQREARPALLSLRFPKPGDHLRPTYNNMDVYVGARTFRERKAELTSRKYA 660

661 LFSVINYERARRPGILGASVGLDDIHRRAWRTEVYLRVAQDPPPELYKVVDTGAYTI 720

661 LFSVINYERARRPGILGASVGLDDIHRRAWRTEVYLRVAQDPPPELYKVVDTGAYTI 720

721 PQDRLETEVIAISKPQNTYCVRRAVVAQKAAGHIVRKFKSHVSTLTLQPMRQFV AHL 780

721 PQDRLETEVIAISKPQNTYCVRRAVVAQKAAGHIVRKFKSHVSTLTLQPMRQFV AHL 780

781 QETSPRLDAVVIQDSSLNEAASSGLFDLRFMCHAVTRGKSYVQCGIPGSI1STL 840

781 QETSPRLDAVVIQDSSLNEAASSGLFDLRFMCHAVTRGKSYVQCGIPGSI1STL 840

841 LCSLCYGDGMENKLPAIGIRDGLLRLVDFLTPHILTHAKTFLRTLRGVPYGCYVNL 900

841 LCSLCYGDGMENKLPAIGIRDGLLRLVDFLTPHILTHAKTFLRTLRGVPYGCYVNL 900

901 RKTIVNPFYDEALGGTAVQMPAHGLPPWCGLLLDTRTLEYQSDYSSYARTSIRASLT 960

901 RKTIVNPFYDEALGGTAVQMPAHGLPPWCGLLLDTRTLEYQSDYSSYARTSIRASLT 960

RESULT 2

US-08-974-549-A-2

Sequence 2, Application US/08974549A

Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

CITY: San Francisco

ZIP: 94111-38314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974, 549A

FILING DATE: 19-NOV-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724, 643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974, 549A

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846, 017

FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851, 843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854, 050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/911, 312

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912, 951

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/915, 503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: NO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17885  
 FILING DATE: 01-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Apple, Randolph Ted  
 REGISTRATION NUMBER: 3,6,429  
 REFERENCE/DOCKET NUMBER: 015389-0-02610US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEX/FAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-974-549A-2

Query Match 100.0%; Score 5961; DB 3; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Gaps 0;

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 Db 1 MPRAPCRAYTSLRSHREVLPLATVRLGPQCMWRVQGDPAFAFRALVAVQLCVPW 60

QY 61 DARPPPAAPSPRQVSCLKEVAVLQLRCLERGAKTVLAFGAFALLDARGSPPEAFTTSYR 120  
 Db 61 DARPPPAAPSPRQVSCLKEVAVLQLRCLERGAKTVLAFGAFALLDARGSPPEAFTTSYR 120

QY 121 SYLPNTVTDALRGSGAWGLLRLRGDVLTHLLARCAFLVAPSCAYQVGPPLYQLGA 180  
 Db 121 SYLPNTVTDALRGSGAWGLLRLRGDVLTHLLARCAFLVAPSCAYQVGPPLYQLGA 180

QY 181 ATQAREPPHAGSPRERLGCBAWNNSVREAGVPLGPAPGARRGSGASRSLPLPKRPR 240  
 Db 181 ATQAREPPHAGSPRERLGCBAWNNSVREAGVPLGPAPGARRGSGASRSLPLPKRPR 240

QY 241 GAAPEPRTPIQGGSMAHPGTRGSDRGFCVSPARPAEATSLLEGALSCTRISHPSVG 300  
 Db 241 GAAPEPRTPIQGGSMAHPGTRGSDRGFCVSPARPAEATSLLEGALSCTRISHPSVG 300

QY 301 RQHHAGPPSTSRRPPWDTCPVPTAETKHFLYSSSDKEQLRSPFLSSLRPSLTGARRL 360  
 Qy 301 RQHHAGPPSTSRRPPWDTCPVPTAETKHFLYSSSDKEQLRSPFLSSLRPSLTGARRL 360

QY 361 VETIFGSRPMPGTPRLPPLPQYWMQMPFLLELGHNAQCPCPGVLLKTHCPRAVTT 420  
 Db 361 VETIFGSRPMPGTPRLPPLPQYWMQMPFLLELGHNAQCPCPGVLLKTHCPRAVTT 420

QY 421 PAAGVCAREKQDGSYAAPEEEDTDPRLVQLLQHSSPMQVYGFYTRACLRVPPGLWGS 480  
 Db 421 PAAGVCAREKQDGSYAAPEEEDTDPRLVQLLQHSSPMQVYGFYTRACLRVPPGLWGS 480

QY 481 RHNERFLRNTKKFISLGKHAKLSQLBLTWSRDCAWLRSRPGVGCVPAAEHRLREBI 540  
 Db 481 RHNERFLRNTKKFISLGKHAKLSQLBLTWSRDCAWLRSRPGVGCVPAAEHRLREBI 540

QY 541 LAKPFLWLMSSVYVVELRSFYYTETFOKNRLFFYRKSWKLSQIGSITRQLKRVQLRE 600  
 Db 541 LAKPFLWLMSSVYVVELRSFYYTETFOKNRLFFYRKSWKLSQIGSITRQLKRVQLRE 600

QY 601 LSEAETVRQHREARPALLTSRLFIPKPGLRPIVNMDDYVCAUTRERKAERLTSRVKA 660  
 Db 601 LSEAETVRQHREARPALLTSRLFIPKPGLRPIVNMDDYVCAUTRERKAERLTSRVKA 660

QY 661 LFSVINYERARRPGLGASVGLDDTHRATFTVIRVRAQDPPPEYFVKVDVTGAYDTI 720  
 Db 661 LFSVINYERARRPGLGASVGLDDTHRATFTVIRVRAQDPPPEYFVKVDVTGAYDTI 720

QY 721 PQDRLETEVIASIKPONTYCVRYYAVVQKAHGHYRKAFISHVSTLTDLOPMMQFVAHL 780  
 Db 721 PQDRLETEVIASIKPONTYCVRYYAVVQKAHGHYRKAFISHVSTLTDLOPMMQFVAHL 780

QY 781 QETSPURDAVIEQSSLINEASSSGLFDVFLRFMCHAVTRGKSYVOCOGIPOGSILSTL 840  
 Db 781 QETSPURDAVIEQSSLINEASSSGLFDVFLRFMCHAVTRGKSYVOCOGIPOGSILSTL 840

QY 841 LCSLCYGDMEKLNKLAGIRRDGLLRLVDDFLVTPHLTHAKTFRLTVLRCPEYCCVNL 900  
 Db 841 LCSLCYGDMEKLNKLAGIRRDGLLRLVDDFLVTPHLTHAKTFRLTVLRCPEYCCVNL 900

QY 901 RKTUVNFPVDEAUGTAFVQMPAHLFPMCGLILDTRLTEQSDYSSARTSBRASLTF 960  
 Db 901 RKTUVNFPVDEAUGTAFVQMPAHLFPMCGLILDTRLTEQSDYSSARTSBRASLTF 960

QY 961 NRGPKAGRNMRKLFGVLRKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACTVQLQP 1020  
 Db 961 NRGPKAGRNMRKLFGVLRKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACTVQLQP 1020

QY 1021 FHQQWKNPTEFLRIVSITASLCLCSYLSILKAKNAGMSLGAKAAGGLPSEAVOWLCHOAFL 1080  
 Db 1021 FHQQWKNPTEFLRIVSITASLCLCSYLSILKAKNAGMSLGAKAAGGLPSEAVOWLCHOAFL 1080

QY 1081 KLTRHRVTVPILLGSLRATAOTQLSRKLPGTTLALEAAANPALSDFKTLLD 1132  
 Db 1081 KLTRHRVTVPILLGSLRATAOTQLSRKLPGTTLALEAAANPALSDFKTLLD 1132

RESULT 3  
 US-08-854-050-225  
 Sequence 225; Application US/08854050  
 Patent No. 6,618,816

GENERAL INFORMATION:  
 APPLICANT: Cech, Thomas R.  
 APPLICANT: Lingner, Joachim  
 APPLICANT: Nakamura, Toru  
 APPLICANT: Chapman, Karen B.  
 APPLICANT: Morin, Gregg B.  
 APPLICANT: Harley, Calvin  
 APPLICANT: Andrews, William H.  
 TITLE OF INVENTION: Number of Sequences: 225  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, 8th Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States of America  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/854,050  
 FILING DATE: 09-MAY-1997  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/851,843  
 FILING DATE: 06-MAY-1997  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/846,017  
 FILING DATE: 25-APR-1997  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/851,843  
 FILING DATE: 01-OCT-1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429  
 REFERENCE/DOCKET NUMBER: 015389-002930US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 225:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-09-054-050-225

Query Match Best Local Similarity 100.0%; Score 5961; DB 3; Length 1132;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPPAPRCAVRSLSRSHYREVPLATFVRLGPOGMVLVQGDPAATRALVAQCLVCVPW 60  
 Db 1 MPPAPRCAVRSLSRSHYREVPLATFVRLGPOGMVLVQGDPAATRALVAQCLVCVPW 60

Qy 61 DAPPPAAPSFRQVSCKEVLAQVLRQICERGAKNVLAFGAIIDGARGGPPBAAFTTSVR 120  
 Db 61 DAPPPAAPSFRQVSCKEVLAQVLRQICERGAKNVLAFGAIIDGARGGPPBAAFTTSVR 120

Qy 121 SYPNPTVTDALRGSGANGLRLRGDDVLYHLLARCALFVLYAPSCAYQVCGPPLYOLGA 180  
 Db 121 SYPNPTVTDALRGSGANGLRLRGDDVLYHLLARCALFVLYAPSCAYQVCGSPLYQLGA 180

Qy 181 ATQARPPHASSGRRLGCERAWNHSTREAGVPLGLDAPGARRGGASRSPLPKRPRR 240  
 Db 181 ATQARPPHASSGRRLGCERAWNHSTREAGVPLGLDAPGARRGGASRSPLPKRPRR 240

Qy 241 GAAPEPPTVPGGSSWAHPGTRGSDRGFCVVSPPARAEATSLEGALSGSTRSHPSVG 300  
 Db 241 GAAPEPPTVPGGSSWAHPGTRGSDRGFCVVSPPARAEATSLEGALSGSTRSHPSVG 300

Qy 301 ROHHAGPSTSREPRPDTPCPVVAETKHFLLYSSGDXKEQLRPSFLSSRLPSLTGARRL 360  
 Db 301 ROHHAGPSTSREPRPDTPCPVVAETKHFLLYSSGDXKEQLRPSFLSSRLPSLTGARRL 360

Qy 361 VETTLYGSRPWNNGTPARLPRFQRYWQMRPFLFELLLGHNACPYGLLKHCPPLRAAVT 420  
 Db 361 VETTLYGSRPWNNGTPARLPRFQRYWQMRPFLFELLLGHNACPYGLLKHCPPLRAAVT 420

Qy 421 PAGAVCAREKPOGSVAAPEEEDTPRLVQLLRQHSSPWQYQGYVACRLRRLVPPGLWGS 480  
 Db 421 PAGAVCAREKPOGSVAAPEEEDTPRLVQLLRQHSSPWQYQGYVACRLRRLVPPGLWGS 480

Qy 481 RHNERFLRNTKFKISLGKHAKLSQLQETLWMSYRDCAWLRSRGVCPAAEHRLREEI 540  
 Db 481 RHNERFLRNTKFKISLGKHAKLSQLQETLWMSYRDCAWLRSRGVCPAAEHRLREEI 540

Qy 541 LAKELILWMSYVWLLRSFIVTETTPQRQLFFRKWSKLQSJGROHLKRVQLRE 600  
 Db 541 LAKELILWMSYVWLLRSFIVTETTPQRQLFFRKWSKLQSJGROHLKRVQLRE 600

Qy 601 LSEAEYRQHREARPALITSRLRFIPKDGURPIVNMDDYVWVQGARTFREKZEARLTSRVKA 660  
 Db 601 LSEAEYRQHREARPALITSRLRFIPKDGURPIVNMDDYVWVQGARTFREKZEARLTSRVKA 660

Qy 661 IFSVLYNERYARRPGLGASVGLDDTHRMTTEVLVRQAQPPPELYFKVDTGAYDTI 720  
 Db 661 IFSVLYNERYARRPGLGASVGLDDTHRMTTEVLVRQAQPPPELYFKVDTGAYDTI 720

Qy 721 BQDRLEVIASIKPONTYCYRRAYVQKAHGHYKAFKSHVSTTDQYMRQV AHL 780  
 Db 721 BQDRLEVIASIKPONTYCYRRAYVQKAHGHYKAFKSHVSTTDQYMRQV AHL 780

Qy 781 QETSPRDVAYTEQSSLNEASGLFDVFLRFMCHHAIRGKSYVQCOGIPQGSILSTL 840  
 Db 781 QETSPRDVAYTEQSSLNEASGLFDVFLRFMCHHAIRGKSYVQCOGIPQGSILSTL 840

RESULT 4  
 US-09-430-323-225  
 ; Sequence 225, Application US/09430323  
 ; Patent No. 6309867, Application US/09430323  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cech, Thomas R.  
 ; Lingner, Joachim  
 ; Nakamura, Toru  
 ; Chapman, Karen B.  
 ; Morin, Gregg B.  
 ; Harley, Calvin  
 ; Andrews, William H.  
 ; TITLE OF INVENTION: No. 6309867 el Telomerase  
 ; NUMBER OF SEQUENCES: 225  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, 8th Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States of America  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/430,323  
 ; FILING DATE: 29-Oct-1999  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/854,050  
 ; FILING DATE: 09-MAY-1997  
 ; APPLICATION NUMBER: US 08/851,843  
 ; FILING DATE: 06-MAY-1997  
 ; APPLICATION NUMBER: US 08/846,017  
 ; FILING DATE: 25-APR-1997  
 ; APPLICATION NUMBER: US 08/844,419  
 ; FILING DATE: 18-APR-1997  
 ; APPLICATION NUMBER: US 08/724,643  
 ; FILING DATE: 01-OCT-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Apple, Randolph T.  
 ; REGISTRATION NUMBER: 36,129  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; INFORMATION FOR SEQ ID NO: 225:  
 ; SEQUENCE CHARACTERISTICS:  
 ; TYPE: amino acids  
 ; LENGTH: 1132 amino acids  
 ; TYPE: amide  
 ; SEQUENCE:  
 ; 1132 amino acids

TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 225;  
 US-09-430-323-225

Query Match 100.0%; Score 5961; DB 3; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Gaps 0;  
 Db 1 MPRAPRCAVSLRSLRSHREVLPLATFVRIGPQGRVLVRGDPAAFRALVAQCLVCPW 60  
 Db 1 MPRAPRCAVSLRSLRSHREVLPLATFVRIGPQGRVLVRGDPAAFRALVAQCLVCPW 60

Qy 61 DARPPPAPSPRQVSCIKEVAVLQLRCLERGAKNVLAFGFALLDARGGPEAFTTSYR 120  
 Db 61 DARPPPAPSPRQVSCIKEVAVLQLRCLERGAKNVLAFGFALLDARGGPEAFTTSYR 120  
 Qy 121 SYLPNTVTDALRGSGAWGLLRLVHLLARCLFVLPAPSCAYQVCGPPLYQLGA 180  
 Db 121 SYLPNTVTDALRGSGAWGLLRLVHLLARCLFVLPAPSCAYQVCGPPLYQLGA 180

Qy 181 ATQRPPPHAGSPRRLGCEAWNHSREAGVPLGIAPGARRGGSASISLPLPKPRRR 240  
 Db 181 ATQRPPPHAGSPRRLGCEAWNHSREAGVPLGIAPGARRGGSASISLPLPKPRRR 240

Qy 241 GAAPEPRTPIQGQSHAHAPGRTRGPSPDRGFCVWSPARPAAEATSLLEGALSCTRISHPSVG 300  
 Db 241 GAAPEPRTPIQGQSHAHAPGRTRGPSPDRGFCVWSPARPAAEATSLLEGALSCTRISHPSVG 300

Qy 301 ROHHAGPPSTSRPPWDTPCPVTAETKFLYSSSDKEQLRPSFLSSLRPSLTGARRL 360  
 Db 301 ROHHAGPPSTSRPPWDTPCPVTAETKFLYSSSDKEQLRPSFLSSLRPSLTGARRL 360

Qy 361 VETIFGSRPWPNGTTRPLPFLQTPWMQRLFLFELGNHQCPYGVLLKTHCPRAVFT 420  
 Db 361 VETIFGSRPWPNGTTRPLPFLQTPWMQRLFLFELGNHQCPYGVLLKTHCPRAVFT 420

Qy 421 PAAGVCAREKPOGSVAAPEEBDTDPRLVQFLQFLRQHSSPMQVYGFYRACLRLVPGFLWGS 480  
 Db 421 PAAGVCAREKPOGSVAAPEEBDTDPRLVQFLRQHSSPMQVYGFYRACLRLVPGFLWGS 480

Qy 481 RHNERFLRNTYKKFISIGKHAKLSQLLTWMSVRDCAWLRRSPGVGCVPAAEHRLREI 540  
 Db 481 RHNERFLRNTYKKFISIGKHAKLSQLLTWMSVRDCAWLRRSPGVGCVPAAEHRLREI 540

Qy 541 LAKFLFLWMSYYVVELRSFYYVTEFTFQKNRLFFYTRKSTWSKLSQIGIQRQLKRVQRE 600  
 Db 541 LAKFLFLWMSYYVVELRSFYYVTEFTFQKNRLFFYTRKSTWSKLSQIGIQRQLKRVQRE 600

Qy 601 LSEAEVQRHREARPALLTSRLRPIPKDGLRPIVNMDDYVGARTREKERAERTSRVKA 660  
 Db 601 LSEAEVQRHREARPALLTSRLRPIPKDGLRPIVNMDDYVGARTREKERAERTSRVKA 660

Qy 721 PQDRLTVETASIKPONTYCYRRAVYQKAAGHRYKRAFKSHVSTLTDQPYMRFVAHL 780  
 Db 721 PQDRLTVETASIKPONTYCYRRAVYQKAAGHRYKRAFKSHVSTLTDQPYMRFVAHL 780

Qy 781 QETSPRLDAVVIQESSLNEASSGLFDVLFMCHHAVRFRGKSYVQCGQIPOGSILSTL 840  
 Db 781 QETSPRLDAVVIQESSLNEASSGLFDVLFMCHHAVRFRGKSYVQCGQIPOGSILSTL 840

Qy 841 LCLSLCYGDMDENKLFGAGRDRGFLRLVDFLFTVPHTHAKTFRLTVEQSDSYSTARTSIRASLTF 900  
 Db 841 LCLSLCYGDMDENKLFGAGRDRGFLRLVDFLFTVPHTHAKTFRLTVEQSDSYSTARTSIRASLTF 900

Qy 901 RKTIVNFPVDEBALGCTAIVOMPAHGLFPNGLGLLIDTRTLEQSDSYSTARTSIRASLTF 960  
 Db 901 RKTIVNFPVDEBALGCTAIVOMPAHGLFPNGLGLLIDTRTLEQSDSYSTARTSIRASLTF 960

Qy 961 NRGFFAKGRNMNRKLFGLVLRKCHSLFLDIQVNSLQTVCTNIYKLLQAOYRFHACVQLQP 1020  
 Db 961 NRGFFAKGRNMNRKLFGLVLRKCHSLFLDIQVNSLQTVCTNIYKLLQAOYRFHACVQLQP 1020

Qy 1021 FHQQWKNPTEFLRIVSITASLCYTSILKAKNAGMSLGAKAAGLPLPSEAVQWLQHQAFL 1080  
 Db 1021 FHQQWKNPTEFLRIVSITASLCYTSILKAKNAGMSLGAKAAGLPLPSEAVQWLQHQAFL 1080

Qy 1081 KLTTRVTVYPLLGSURTAQTQLSRKLPGTTLALEAAANPALPDPDKTLLD 1132  
 Db 1081 KLTTRVTVYPLLGSURTAQTQLSRKLPGTTLALEAAANPALPDPDKTLLD 1132

RESULT 5  
 US-09-128-354-2  
 Sequence 2, Application US/09128354  
 Patent No. 6337200  
 GENERAL INFORMATION:  
 APPLICANT: Morin, Gregg B.  
 APPLICANT: Geron Corporation  
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants  
 FILE REFERENCE: 015389-003310US  
 CURRENT APPLICATION NUMBER: US/09/128-354  
 CURRENT FILING DATE: 1998-08-03  
 EARLIER APPLICATION NUMBER: US 08/851,843  
 EARLIER FILING DATE: 1997-05-06  
 EARLIER APPLICATION NUMBER: US 08/854,050  
 EARLIER FILING DATE: 1997-05-09  
 EARLIER APPLICATION NUMBER: US 08/911,312  
 EARLIER FILING DATE: 1997-08-14  
 EARLIER APPLICATION NUMBER: US 08/912,951  
 EARLIER FILING DATE: 1997-08-14  
 EARLIER APPLICATION NUMBER: US 08/915,503  
 EARLIER FILING DATE: 1997-08-14  
 EARLIER APPLICATION NUMBER: WO PCT/US97/17618  
 EARLIER FILING DATE: 1997-10-01  
 EARLIER APPLICATION NUMBER: WO PCT/US97/17885  
 EARLIER FILING DATE: 1997-10-01  
 EARLIER FILING DATE: 1997-11-19  
 EARLIER APPLICATION NUMBER: US 08/974,584  
 EARLIER FILING DATE: 1997-11-19  
 EARLIER APPLICATION NUMBER: US 09/052,864  
 EARLIER FILING DATE: 1998-03-31  
 NUMBER OF SEQ ID NOS: 21  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 2  
 LENGTH: 1132  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-128-354-2

Qy 1 MPRACRACRARSLSRSHREYREVLPATFVRRLGPQGWRLVORGDPAAFLALVACLIVCPW 60  
 Db 1 MPRACRACRARSLSRSHREYREVLPATFVRRLGPQGWRLVORGDPAAFLALVACLIVCPW 60

Qy 61 DARPDDAAPSFRQSCLSKELVARYLQRLCERGAKNVLAFGFLDARGGPPEAFTTSVR 120  
 Db 61 DARPDDAAPSFRQSCLSKELVARYLQRLCERGAKNVLAFGFLDARGGPPEAFTTSVR 120

Qy 121 SYLPNTVTDALRGSGAWGLLRLVHLLARCAFLFVYQVCGPPIYQIGA 180  
 Db 121 SYLPNTVTDALRGSGAWGLLRLVHLLARCAFLFVYQVCGPPIYQIGA 180

Qy 181 ATQAPPHASGSPRRLGCEAWNHSREAGVPLGLPAPARRGGSASRSLPLPKPRRR 240  
 Db 181 ATQAPPHASGSPRRLGCEAWNHSREAGVPLGLPAPARRGGSASRSLPLPKPRRR 240

Qy 241 GAAPPERTPVQGQSWAHPGPRTGSDRGFCVPSRPARPABEATLEGALSGTRSHPSVG 300

Db	241	GAAPPERTPVGGSWAHPGRTGPSSRGFCVSPARPAEATSLLEGALSSTRHSHPSVG	300	;	PRIOR FILING DATE: 1998-03-31
Qy	301	RQHAGPESTSREPRPDRTPCPVYATKHFYSSGKEQRPSPFLSSRPLTGTARRL	360	;	PRIOR FILING DATE: 1999-03-30
Db	301	RQHAGPESTSREPRPDRTPCPVYATKHFYSSGKEQRPSPFLSSRPLTGTARRL	360	;	NUMBER OF SEQ ID NOS: 2
Qy	361	VERIFLSSRPMNGTPTPLRPLPDRQTYWQMRPLFLELGNHACQPCVLLKTHCPRAVY	420	;	SOFTWARE: PatentIn Ver. 2.0
Db	361	VERIFLSSRPMNGTPTPLRPLPDRQTYWQMRPLFLELGNHACQPCVLLKTHCPRAVY	420	;	SEQ ID NO: 2
Qy	421	PAGVCAREKPOSSVAPEEEEDTDPRLVQLRQHSSPWQVYGFYRCAFLRLVPGLGWS	480	;	LENGTH: 1132
Db	421	PAGVCAREKPOSSVAPEEEEDTDPRLVQLRQHSSPWQVYGFYRCAFLRLVPGLGWS	480	;	TYPE: PRT
Qy	481	REINERRPLRNTKFKISGKHAKLSQLELTWMNSVDCAWLRSRPGVYCVAEERLREEI	540	;	ORGANISM: Homo sapiens
Db	481	REINERRPLRNTKFKISGKHAKLSQLELTWMNSVDCAWLRSRPGVYCVAEERLREEI	540	;	US-09-675-321-2
Qy	541	LAKFILHMLMSVYVVELRSFFVYETTFQKNRLFFYRKSWSKQCGISGRQHLKRVQRE	600	;	US-09-675-321-2
Db	541	LAKFILHMLMSVYVVELRSFFVYETTFQKNRLFFYRKSWSKQCGISGRQHLKRVQRE	600	;	Query Match 100.0% ; Score 5961; DB 4 ; Length 1132;
Qy	601	LSEAEVTRQHREARPALLTSRLRFKPDGLRPIVNMDDYVYVARTFRREKRAERLTSRYKA	660	;	Best Local Similarity 100.0% ; Pred. No. 0;
Db	601	LSEAEVTRQHREARPALLTSRLRFKPDGLRPIVNMDDYVYVARTFRREKRAERLTSRYKA	660	;	Mismatches 0 ; Indels 0 ; Gaps 0 ;
Qy	661	LFSVNLNEYERARRPGLIGASVIGLDDHRAWTRFVLRRAODDPPLFVYRVDTGAYDTI	720	;	Matches 1132 ; Conservative 0 ;
Db	661	LFSVNLNEYERARRPGLIGASVIGLDDHRAWTRFVLRRAODDPPLFVYRVDTGAYDTI	720	;	Score 5961; DB 4 ; Length 1132;
Qy	721	QDRLTVEIASLIKPONTYCVRYYAVQKAHGHYRKAFKSHVSTLTDQYRQFV AHL	780	;	Query Match 100.0% ; Score 5961; DB 4 ; Length 1132;
Db	721	QDRLTVEIASLIKPONTYCVRYYAVQKAHGHYRKAFKSHVSTLTDQYRQFV AHL	780	;	Best Local Similarity 100.0% ; Pred. No. 0;
Qy	781	QETSPRDVAVIEQSSSLNEASMSGLEDFVFRMCHAVATRGSYVOCGIPOQSITSL	840	;	Mismatches 0 ; Indels 0 ; Gaps 0 ;
Db	781	QETSPRDVAVIEQSSSLNEASMSGLEDFVFRMCHAVATRGSYVOCGIPOQSITSL	840	;	Score 5961; DB 4 ; Length 1132;
Qy	841	LCSLCYGDGMENKLFAIGTRIGLRLIYDDTLVTPHLTIAKTFTRLTVGYPEYGCVN L	900	;	Query Match 100.0% ; Score 5961; DB 4 ; Length 1132;
Db	841	LCSLCYGDGMENKLFAIGTRIGLRLIYDDTLVTPHLTIAKTFTRLTVGYPEYGCVN L	900	;	Best Local Similarity 100.0% ; Pred. No. 0;
Qy	901	RKTYVNFYVEDEAGTAGTAAVQMPAHGLFPNCGLLDTTRLEQSDYSSYARTSIRASITF	960	;	Mismatches 0 ; Indels 0 ; Gaps 0 ;
Db	901	RKTYVNFYVEDEAGTAGTAAVQMPAHGLFPNCGLLDTTRLEQSDYSSYARTSIRASITF	960	;	Score 5961; DB 4 ; Length 1132;
Qy	961	NRGFKAGRMGRKLEPGVLRKCHSIFLDLQVNSLQTCNTIYKULLOAYRFHACVLQLP	1020	;	Query Match 100.0% ; Score 5961; DB 4 ; Length 1132;
Db	961	NRGFKAGRMGRKLEPGVLRKCHSIFLDLQVNSLQTCNTIYKULLOAYRFHACVLQLP	1020	;	Best Local Similarity 100.0% ; Pred. No. 0;
Qy	1021	FHQQWIKNPFFLRTISDTASLCYTSILAKNAGNLSGKGAAGPLPSAVQWICHQFL	1080	;	Mismatches 0 ; Indels 0 ; Gaps 0 ;
Db	1021	FHQQWIKNPFFLRTISDTASLCYTSILAKNAGNLSGKGAAGPLPSAVQWICHQFL	1080	;	Score 5961; DB 4 ; Length 1132;
Qy	1081	KLTRHRTVYVPLGSLSLRATQTSRKLPGTTTALEAAANPALPSDFKTTLD	1132	;	Query Match 100.0% ; Score 5961; DB 4 ; Length 1132;
Db	1081	KLTRHRTVYVPLGSLSLRATQTSRKLPGTTTALEAAANPALPSDFKTTLD	1132	;	Best Local Similarity 100.0% ; Pred. No. 0;
Qy	1132	;	;	;	;
Db	1132	;	;	;	;
Qy	6	;	;	;	;
Db	6	;	;	;	;
Qy	661	LFSVNLNEYERARRPGLIGASVIGLDDTHRAWTRFVLRRAODDPPLFVYRVDTGAYDTI	720	;	QDRLTVEIASLIKQNTYCVRYYAVQKAHGHYRKAFKSHVSTLTDQYRQFV AHL
Db	661	LFSVNLNEYERARRPGLIGASVIGLDDTHRAWTRFVLRRAODDPPLFVYRVDTGAYDTI	720	;	QDRLTVEIASLIKQNTYCVRYYAVQKAHGHYRKAFKSHVSTLTDQYRQFV AHL
Qy	721	QDRLTVEIASLIKQNTYCVRYYAVQKAHGHYRKAFKSHVSTLTDQYRQFV AHL	780	;	QDRLTVEIASLIKQNTYCVRYYAVQKAHGHYRKAFKSHVSTLTDQYRQFV AHL
Db	721	QDRLTVEIASLIKQNTYCVRYYAVQKAHGHYRKAFKSHVSTLTDQYRQFV AHL	780	;	QDRLTVEIASLIKQNTYCVRYYAVQKAHGHYRKAFKSHVSTLTDQYRQFV AHL
Qy	781	QETSPRDVAVIEQSSSLNEASMSGLEDFVFRMCHAVATRGSYVOCGIPOQSILSTL	840	;	QETSPRDVAVIEQSSSLNEASMSGLEDFVFRMCHAVATRGSYVOCGIPOQSILSTL
Db	781	QETSPRDVAVIEQSSSLNEASMSGLEDFVFRMCHAVATRGSYVOCGIPOQSILSTL	840	;	QETSPRDVAVIEQSSSLNEASMSGLEDFVFRMCHAVATRGSYVOCGIPOQSILSTL
Qy	841	LCSLCYGDGMENKLFAIGTRIGLRLIYDDTLVTPHLTIAKTFTRLTVGYPEYGCVN L	900	;	QETSPRDVAVIEQSSSLNEASMSGLEDFVFRMCHAVATRGSYVOCGIPOQSILSTL

RESULT 6

US-09-675-321-2

; Sequence 2, Application US/09675321

; Patent No. 6440735

; GENERAL INFORMATION:

; APPLICANT: Gaera Federico C.A.

; APPLICANT: Geron Corporation

; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune

; TITLE OF INVENTION: Response to a Telomerase Antigen

; FILE REFERENCE: 015389-00350PC

; CURRENT APPLICATION NUMBER: US/09/675.321

; CURRENT FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/112,006

Db 841 LCSLCYGDMEKLFAGIRRDGILLRLVDDFLFLVTPHILTHAKTFLRLTVRGPEYGVNL 900  
 Qy 901 RKTIVNFPVEDEALGTAFAVOMPAHGLFPWCGLLDRTLVEQSDYSYARTSIRASLTF 960  
 Db 901 RKTIVNFPVEDEALGTAFAVOMPAHGLFPWCGLLDRTLVEQSDYSYARTSIRASLTF 960  
 Qy 961 NRGFKAAGRNMERKLFLGFLKCHSLFLDQVNSLQVCTNYYKILLQATRFHACVQLP 1020  
 Db 961 NRGFKAAGRNMERKLFLGFLKCHSLFLDQVNSLQVCTNYYKILLQATRFHACVQLP 1020  
 Qy 1021 FHQQVWKNPTEFLRVISDTASLCSYSLKAKNAGMSLGAKGAAGLPSEAYQWLQHAFIL 1080  
 Db 1021 FHQQVWKNPTEFLRVISDTASLCSYSLKAKNAGMSLGAKGAAGLPSEAYQWLQHAFIL 1080  
 Qy 1081 KLTRHRVTVYPLGLSRTAQTLQSLRKPQTTLAEEAANPALPSDFKTLID 1132  
 Db 1081 KLTRHRVTVYPLGLSRTAQTLQSLRKPQTTLAEEAANPALPSDFKTLID 1132

RESULT 7  
 US-09-052-919-2  
 Sequence 2, Application US/09052919  
 GENERAL INFORMATION:  
 Patent No. 6444650  
 APPLICANT: Cech, Thomas R.  
 APPLICANT: Lingner, Joachim  
 APPLICANT: Nakamura, Toru  
 APPLICANT: Chapman, Karen B.  
 APPLICANT: Morin, Gregg B.  
 APPLICANT: Harvey, Calvin B.  
 APPLICANT: Andrews, William H.  
 TITLE OF INVENTION: Antisense Compositions for Detecting and  
 Title of Invention: Antisense Compositions for Detecting and  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/052,919  
 FILING DATE: 31-MAY-1998  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/724,613  
 FILING DATE: 01-OCT-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/844,419  
 FILING DATE: 18-APR-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/846,017  
 FILING DATE: 25-APR-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/851,843  
 FILING DATE: 06-MAY-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/854,050  
 FILING DATE: 09-MAY-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/911,312  
 FILING DATE: 14-AUG-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/912,931  
 FILING DATE: 14-AUG-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/974,549  
 FILING DATE: 19-NOV-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/974,584  
 FILING DATE: 19-NOV-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US97/17618  
 FILING DATE: 01-OCT-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US97/17885  
 FILING DATE: 01-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parent, Annette S.  
 REGISTRATION NUMBER: 42,058  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-052-919-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Query 1 MPRAPCRAVRSLLSRYREVLPATEFVRFLQGQFWRLVQGDPAFRLVYQCLVCPW 60  
 Db 1 MPRAPCRATRSLLSRYREVLPATEFVRFLQGQFWRLVQGDPAFRLVYQCLVCPW 60  
 Qy 61 DARPAAAPSPRSQVSCLEKILVQLRCLERGAKVLAFLGARGGPPEAFTTSVR 120  
 Db 61 DARPAAAPSPRSQVSCLEKILVQLRCLERGAKVLAFLGARGGPPEAFTTSVR 120  
 Qy 61 DARPAAAPSPRSQVSCLEKILVQLRCLERGAKVLAFLGARGGPPEAFTTSVR 120  
 Db 121 SYLPNTVTDALRGSGAWGLLRLRMLARCALFVLYVAPSCAYQVGPPLYQLGA 180  
 Db 121 SYLPNTVTDALRGSGAWGLLRLRMLARCALFVLYVAPSCAYQVGPPLYQLGA 180  
 Qy 181 ATQAPPAPHASGPRLGCRAMWNEVSREAGVPLPAPARRGGSASESLPLPKRPRR 240  
 Db 181 ATQAPPAPHASGPRLGCRAMWNEVSREAGVPLPAPARRGGSASESLPLPKRPRR 240  
 Qy 241 GAAPEPERTPVQGGSWAHPGTRGSDRGFCVVSAPRABEATSGTRASHPSVG 300  
 Db 241 GAAPEPERTPVQGGSWAHPGTRGSDRGFCVVSAPRABEATSGTRASHPSVG 300  
 Qy 301 RQHAGPPSTSRRPRPWDTCPPPYAAETKHFLLYSSGDKEOLRSPFLLSSLRPSTGARRL 360  
 Db 301 RQHAGPPSTSRRPRPWDTCPPPYAAETKHFLLYSSGDKEOLRSPFLLSSLRPSTGARRL 360  
 Qy 361 VETIFGSRSPWMPGPTRRPLPQBYQWPLFELLGNHAQCPYVLLKTHCPRAAVT 420  
 Db 361 VETIFGSRSPWMPGPTRRPLPQBYQWPLFELLGNHAQCPYVLLKTHCPRAAVT 420  
 Qy 421 PAAGYCAREKPGQSYAAPEEEEDTPRRLVQPLRQHSSPWOYGYFRACLRLVPPGLWGS 480  
 Db 421 PAAGYCAREKPGQSYAAPEEEEDTPRRLVQPLRQHSSPWOYGYFRACLRLVPPGLWGS 480  
 Qy 481 RHNERRFLRNTKKPISLGKHKAKLSQLQELTWMKMSYRDCAFLRSPGIVGCVPAAEHLREEI 540  
 Db 481 RHNERRFLRNTKKPISLGKHKAKLSQLQELTWMKMSYRDCAFLRSPGIVGCVPAAEHLREEI 540  
 Qy 541 LAKFELHMLMSVYVWELLRSPPYVETTETFQKNRFLFYYRKSVWSKLOSIGRQHLLKVQVLR 600  
 Db 541 LAKFELHMLMSVYVWELLRSPPYVETTETFQKNRFLFYYRKSVWSKLOSIGRQHLLKVQVLR 600  
 Qy 601 LSEAEVQHREARPAALTSRLRFPKDGLRPIVNMYYVGAARTFREKRAERLTTSRVKA 660

601 LSEEVVRQREARPALLSRLRFKPKDGSRPTYNNMDYVGARTFRKEAELTSRVKA 660  
 661 LFSVLYNVEARRPGLLGASVYGLDDIHRRAWTRPFLVRAQDPPPELYFVFKDVTGAYDTI 720  
 661 LFSVLYNVEARRPGLLGASVYGLDDIHRRAWTRPFLVRAQDPPPELYFVFKDVTGAYDTI 720  
 721 PQDLTEVIASIIKPQNTYCVRVYAVVOKAAGHVRKAFKSHYSTLTLQPYNMQFYAH 780  
 721 PQDLTEVIASIIKPQNTYCVRVYAVVOKAAGHVRKAFKSHYSTLTLQPYNMQFYAH 780  
 781 QETSPRLDRAVVEQSS1NEASSGLDFYLFRFCHHABIRGKSYTQCGQ1DQGS1LST 840  
 781 QETSPRLDRAVVEQSS1NEASSGLDFYLFRFCHHABIRGKSYTQCGQ1DQGS1LST 840  
 841 LCSUCYGYMENKLQFAGIRDGLLRLVDFLLVTPHILTHATKFLRLVRYGPEYGVNL 900  
 841 LCSUCYGYMENKLQFAGIRDGLLRLVDFLLVTPHILTHATKFLRLVRYGPEYGVNL 900  
 901 RKTIVNNFPEDEALGGTAFVQMPAHLFPMCGLLDTRLEQSDYSSYARTSIRASLTF 960  
 901 RKTIVNNFPEDEALGGTAFVQMPAHLFPMCGLLDTRLEQSDYSSYARTSIRASLTF 960  
 961 NRGFKAGRNMRRKLFGVLRKCHSLFUDLQNSLQTYCCTNLYKILIJQAYRFHACULQP 1020  
 961 NRGFKAGRNMRRKLFGVLRKCHSLFUDLQNSLQTYCCTNLYKILIJQAYRFHACULQP 1020  
 1021 FHQQVWNQPTFFLVRISDTASLCYSLIKAKNAGMSLGAKGAGPLSEAVOWLCHOAFL 1080  
 1021 FHQQVWNQPTFFLVRISDTASLCYSLIKAKNAGMSLGAKGAGPLSEAVOWLCHOAFL 1080  
 1081 KLTRHRHRYTYVPLGLSLRTAQTQLSRKLPGTTLTALEAANALPSDFKTLID 1132  
 1081 KLTRHRHRYTYVPLGLSLRTAQTQLSRKLPGTTLTALEAANALPSDFKTLID 1132  
 1081 KLTRHRHRYTYVPLGLSLRTAQTQLSRKLPGTTLTALEAANALPSDFKTLID 1132

QY 1 MPRAPCRAYRSLSLIRSHYREVLPPLATEVVRLLGPQCGWRLYORGDPAAFRALVAQCLVCVPN 60  
 Db 1 MPRAPCRAYRSLSLIRSHYREVLPPLATEVVRLLGPQCGWRLYORGDPAAFRALVAQCLVCVPN 60  
 QY 61 DARPPPAAPSFQVSYCLKELVARYLQRLCERGAQKVLAFLGQFALLDARGSPPEAFTTSYR 120  
 Db 61 DARPPPAAPSFQVSYCLKELVARYLQRLCERGAQKVLAFLGQFALLDARGSPPEAFTTSYR 120  
 121 SYLNPNTVTDALRGSGAWGLLRLRGGDVLLHARCALFLVAPSCAYQVCGPPLYQOLGA 180  
 Db 121 SYLNPNTVTDALRGSGAWGLLRLRGGDVLLHARCALFLVAPSCAYQVCGPPLYQOLGA 180  
 QY 181 ATQRPPHASGPRLGERAWHNSVREAGVPLGLPARGARRGGSASRSLPLPKRPRR 240  
 Db 181 ATQRPPHASGPRLGERAWHNSVREAGVPLGLPARGARRGGSASRSLPLPKRPRR 240  
 QY 241 GAAPPEPRTVPGOGSWAHFGRTGPDSRGFCVYSPARAAEATSLLEGALSGTTHSHPSVG 300  
 Db 241 GAAPPEPRTVPGOGSWAHFGRTGPDSRGFCVYSPARAAEATSLLEGALSGTTHSHPSVG 300  
 301 ROHHAGPSTSRRPBPNDTPCPVVAETKHELYSGDKEQLRSSELLSLRPLGARRL 360  
 Db 301 ROHHAGPSTSRRPBPNDTPCPVVAETKHELYSGDKEQLRSSELLSLRPLGARRL 360  
 QY 361 VETFLGSRPMMGTPRPLPRLPQRYQMRPLPLELGNHACQPYGVLLKTHPLRAAVT 420  
 Db 361 VETFLGSRPMMGTPRPLPRLPQRYQMRPLPLELGNHACQPYGVLLKTHPLRAAVT 420  
 QY 421 PANGVACAREKPKQGSVAAPEEEDTPPRLVQRLRQHSSPWOYGFVRACLRLVPGLWGS 480  
 Db 421 PANGVACAREKPKQGSVAAPEEEDTPPRLVQRLRQHSSPWOYGFVRACLRLVPGLWGS 480  
 QY 481 RHNERFLRNTKFKISLGKHKLSSQELTWKMSVRDQAWLRSRPGCVPAAEHRFLREEI 540  
 Db 481 RHNERFLRNTKFKISLGKHKLSSQELTWKMSVRDQAWLRSRPGCVPAAEHRFLREEI 540  
 QY 541 LAKFLHMLSMYYVVEJLRSFFYVTTETFKQNLFFYRKSYRSKLSQSIGIROLHKRYVQRE 600  
 Db 541 LAKFLHMLSMYYVVEJLRSFFYVTTETFKQNLFFYRKSYRSKLSQSIGIROLHKRYVQRE 600  
 QY 541 LAKFLHMLSMYYVVEJLRSFFYVTTETFKQNLFFYRKSYRSKLSQSIGIROLHKRYVQRE 600

RESULT 8  
 Sequence 2, Application US/08912951  
 GENERAL INFORMATION:  
 APPLICANT: Cech, Thomas R.  
 APPLICANT: Liringer, Joachim  
 APPLICANT: Nakamura, Toru  
 APPLICANT: Chapman, Karen B.  
 APPLICANT: Morin, Gregg B.  
 APPLICANT: Harley, Calvin  
 APPLICANT: Andrews, William H.  
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS  
 NUMBER OF SEQUENCES: 335  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, 8th Floor  
 CITY: San Francisco  
 STATE: California  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/912,951  
 FILING DATE: 14-AUG-1997  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/854,050  
 FILING DATE: 09-MAY-1997  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/851,843

Qy 601 LSEAEVQHREARPALLTSRLRFIPKDPGLRPIVNMDDYVGARTFREKERAERLTSRVKA 660  
 Db 601 LSEAEVQHREARPALLTSRLRFIPKDPGLRPIVNMDDYVGARTFREKERAERLTSRVKA 660  
 Qy 661 LFSVNLNEYERARPGLLGASVGLDDTHRAWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720  
 Db 661 LFSVNLNEYERARPGLLGASVGLDDTHRAWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720  
 Qy 721 PODRLTEVIASTIKPQNTYCVRRYAVQKAAGHVRXAFKSHVSTLTDQPYMRQFVAHL 780  
 Db 721 PODRLTEVIASTIKPQNTYCVRRYAVQKAAGHVRXAFKSHVSTLTDQPYMRQFVAHL 780  
 Qy 781 QETSPSLRDAVVIQFQSSNLNEASSGLFVFLFREMCHAVRIRGKSYVQCGTIPQGSTLSTL 840  
 Db 781 QETSPSLRDAVVIQFQSSNLNEASSGLFVFLFREMCHAVRIRGKSYVQCGTIPQGSTLSTL 840  
 Qy 841 LCSLCYGDMEKLFAIGIRRDGLLRLVDFLFLVTPPHLTHAKTFLRLTVRGVPEYGVNL 900  
 Db 841 LCSLCYGDMEKLFAIGIRRDGLLRLVDFLFLVTPPHLTHAKTFLRLTVRGVPEYGVNL 900  
 Qy 901 RKTIVNVPVEDBALGTAFVQMPAHGFPWCGLLDRTTLEVQSDSYARTSIRASLTF 960  
 Db 901 RKTIVNVPVEDBALGTAFVQMPAHGFPWCGLLDRTTLEVQSDSYARTSIRASLTF 960  
 Qy 961 NRGFKAQRNMRKLFGTURKLCHSFLDLQYNSLOTCTNTYKILLQAYRFHACVLQLP 1020  
 Db 961 NRGFKAQRNMRKLFGTURKLCHSFLDLQYNSLOTCTNTYKILLQAYRFHACVLQLP 1020  
 Qy 1021 FHQQWNKNTFPLRVISDTASLCYSTIKAKNAGMSLGAKGAAGPLPSEAYQWLQHQAFL 1080  
 Db 1021 FHQQWNKNTFPLRVISDTASLCYSTIKAKNAGMSLGAKGAAGPLPSEAYQWLQHQAFL 1080  
 Qy 1081 KLTTRHRYTYVPLGSLRTAQFQLSRKLPGTITLTAANPALPSDFKTLID 1132  
 Db 1081 KLTTRHRYTYVPLGSLRTAQFQLSRKLPGTITLTAANPALPSDFKTLID 1132

RESULT 9  
 US-09-402-181B-2  
 Sequence 2, Application US/09402181B  
 Patent No. 6610839  
 GENERAL INFORMATION:  
 APPLICANT: Czech, Thomas R.  
 Lingner, Joachim  
 Nakamura, Toru  
 Chapman, Karen B.  
 Morin, Gregg B.  
 Harley, Calvin B.  
 Andrews, William H.  
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
 NUMBER OF SEQUENCES: 633  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0., Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/402,181B  
 FILING DATE: 29-Sep-1997  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/774,543  
 FILING DATE: 01-OCT-1996  
 APPLICATION NUMBER: US 08/844,419  
 FILING DATE: 18-APR-1997  
 APPLICATION NUMBER: US 08/846,017

Qy 601 LSEAEVQHREARPALLTSRLRFIPKDPGLRPIVNMDDYVGARTFREKERAERLTSRVKA 660  
 Db 601 LSEAEVQHREARPALLTSRLRFIPKDPGLRPIVNMDDYVGARTFREKERAERLTSRVKA 660  
 Qy 661 LFSVNLNEYERARPGLLGASVGLDDTHRAWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720  
 Db 661 LFSVNLNEYERARPGLLGASVGLDDTHRAWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720  
 Qy 721 PODRLTEVIASTIKPQNTYCVRRYAVQKAAGHVRXAFKSHVSTLTDQPYMRQFVAHL 780  
 Db 721 PODRLTEVIASTIKPQNTYCVRRYAVQKAAGHVRXAFKSHVSTLTDQPYMRQFVAHL 780  
 Qy 781 QETSPSLRDAVVIQFQSSNLNEASSGLFVFLFREMCHAVRIRGKSYVQCGTIPQGSTLSTL 840  
 Db 781 QETSPSLRDAVVIQFQSSNLNEASSGLFVFLFREMCHAVRIRGKSYVQCGTIPQGSTLSTL 840  
 Qy 841 LCSLCYGDMEKLFAIGIRRDGLLRLVDFLFLVTPPHLTHAKTFLRLTVRGVPEYGVNL 900  
 Db 841 LCSLCYGDMEKLFAIGIRRDGLLRLVDFLFLVTPPHLTHAKTFLRLTVRGVPEYGVNL 900  
 Qy 901 RKTIVNVPVEDBALGTAFVQMPAHGFPWCGLLDRTTLEVQSDSYARTSIRASLTF 960  
 Db 901 RKTIVNVPVEDBALGTAFVQMPAHGFPWCGLLDRTTLEVQSDSYARTSIRASLTF 960  
 Qy 961 NRGFKAQRNMRKLFGTURKLCHSFLDLQYNSLOTCTNTYKILLQAYRFHACVLQLP 1020  
 Db 961 NRGFKAQRNMRKLFGTURKLCHSFLDLQYNSLOTCTNTYKILLQAYRFHACVLQLP 1020  
 Qy 1021 FHQQWNKNTFPLRVISDTASLCYSTIKAKNAGMSLGAKGAAGPLPSEAYQWLQHQAFL 1080  
 Db 1021 FHQQWNKNTFPLRVISDTASLCYSTIKAKNAGMSLGAKGAAGPLPSEAYQWLQHQAFL 1080  
 Qy 1081 KLTTRHRYTYVPLGSLRTAQFQLSRKLPGTITLTAANPALPSDFKTLID 1132  
 Db 1081 KLTTRHRYTYVPLGSLRTAQFQLSRKLPGTITLTAANPALPSDFKTLID 1132

Query Match 100.0%; Score 5961; DB 4; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MPRAPRCAVTSLSRSHYRVLPLATEFVRLGPQGWLVRQGDPAFRAFLVACLVCPW 60  
 Db 1 MPRAPRCAVTSLSRSHYRVLPLATEFVRLGPQGWLVRQGDPAFRAFLVACLVCPW 60  
 Qy 61 DARPAPPAFSRQSCSKELYVARYLQRLCERGAKNVLAFQFALLIGARGGPPEAFTTSVR 120  
 Db 61 DARPAPPAFSRQSCSKELYVARYLQRLCERGAKNVLAFQFALLIGARGGPPEAFTTSVR 120  
 Qy 121 SYLPNTVTDALRGSGAWGLLRLRGGDDVHLARCALFVLPASCAVQVCPPLQYQLGA 180  
 Db 121 SYLPNTVTDALRGSGAWGLLRLRGGDDVHLARCALFVLPASCAVQVCPPLQYQLGA 180  
 Qy 181 ATQAPRPPHASGPRLGRERAWHNSVREGVPLGLPAPARRGSGASRSLPLPKRPRR 240  
 Db 181 ATQAPRPPHASGPRLGRERAWHNSVREGVPLGLPAPARRGSGASRSLPLPKRPRR 240  
 Qy 241 GAAPERTPVQGGSWAHPERTGBSDRGRFCVVSPPARPAEATLEGALSGTRSHPSVG 300  
 Db 241 GAAPERTPVQGGSWAHPERTGBSDRGRFCVVSPPARPAEATLEGALSGTRSHPSVG 300  
 Qy 301 RQHAGGPSTSRPRPWDTCPPTYAETHFLYSGSGDKEOLRSPLLSRPSTGARRL 360  
 Db 301 RQHAGGPSTSRPRPWDTCPPTYAETHFLYSGSGDKEOLRSPLLSRPSTGARRL 360  
 Qy 361 VETIIGSRWMPGPTRPLPQYWQNRPLFVLLGNAQCPYGVLLKTHCPRAAVT 420  
 Db 361 VETIIGSRWMPGPTRPLPQYWQNRPLFVLLGNAQCPYGVLLKTHCPRAAVT 420  
 Qy 421 PAAGYCAREKPGQSYAAPEBEDTDPRLVQLLRQHSSPQVYGFVACRLRLLVPGLGMS 480  
 Db 421 PAAGYCAREKPGQSYAAPEBEDTDPRLVQLLRQHSSPQVYGFVACRLRLLVPGLGMS 480  
 Qy 481 RHNERFLANTKFKISLGRHAKLSQLELTWKMSYRDLRSLRSVGCVPAAEERLREEI 540  
 Db 481 RHNERFLANTKFKISLGRHAKLSQLELTWKMSYRDLRSLRSVGCVPAAEERLREEI 540  
 Qy 541 LAKFELHWMVYVYVLLRSFVYVETTETTFCRNRLFYRKSVWSKQOSIGRQHLLRQVQRE 600  
 Db 541 LAKFELHWMVYVYVLLRSFVYVETTETTFCRNRLFYRKSVWSKQOSIGRQHLLRQVQRE 600

RESULT 10  
US-09-721-456-2  
Sequence 2, Application US/09721456  
Patent No. 6617110  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,456  
FILING DATE: 22-Nov-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-Nov-1997  
APPLICATION NUMBER: US/08/724,643  
FILING DATE: 01-Oct-1996  
APPLICATION NUMBER: US/08/844,419

Qy 601 LSEAEVYRQHREARPALLTSRLRFIPKPDGLRPIVNMDDYVNGARTPRREKRAERLTSRVKA 660  
Db 601 LSEAEVYRQHREARPALLTSRLRFIPKPDGLRPIVNMDDYVNGARTPRREKRAERLTSRVKA 660  
Qy 661 LFSVNLNEYERARRPGLGASVLGLDDTHRAWTFVLRRAOPPPFLFVKVDVTGAYDTI 720  
Db 661 LFSVNLNEYERARRPGLGASVLGLDDTHRAWTFVLRRAOPPPFLFVKVDVTGAYDTI 720  
Qy 721 PQDRLTTEVIASLIKPONTYCYRRYAVYQKAAGHGHYRKAFKSHVSTLTDIOPYMRQFVAHL 780  
Db 721 PQDRLTTEVIASLIKPONTYCYRRYAVYQKAAGHGHYRKAFKSHVSTLTDIOPYMRQFVAHL 780  
Qy 781 QETSPSLRDAVYIEQSSSLNEAASSGLFDVFLRFMCVHAWRTRGKSYVQCGQIPQGSILSTI 840  
Db 781 QETSPSLRDAVYIEQSSSLNEAASSGLFDVFLRFMCVHAWRTRGKSYVQCGQIPQGSILSTI 840  
Qy 841 LCSLCYGDMDMENKLFAIGIRRDLLRIVDDFLLVTPHLTHAKTFRTLVGVPPEYGCVNLI 900  
Db 841 LCSLCYGDMDMENKLFAIGIRRDLLRIVDDFLLVTPHLTHAKTFRTLVGVPPEYGCVNLI 900  
Qy 901 RKTIVNFPVDEBALGTTAFYQMPAHLFPMCGLJLDTTRTLEVDOSDYSYARTSIRASLTF 960  
Db 901 RKTIVNFPVDEBALGTTAFYQMPAHLFPMCGLJLDTTRTLEVDOSDYSYARTSIRASLTF 960  
Qy 961 NRGFKAAGRNNMRKLRKLFGLVRLKCHSFLDIQVNSLQTVCTNIVKILLQAYRFHACVLQIP 1020  
Db 961 NRGFKAAGRNNMRKLRKLFGLVRLKCHSFLDIQVNSLQTVCTNIVKILLQAYRFHACVLQIP 1020  
Qy 1021 FHQQYWKNPTEFLRVTISDTASLCLYCSILKAKNAGMSLGAKAAGLPSAVQWLQHQAFL 1080  
Db 1021 FHQQYWKNPTEFLRVTISDTASLCLYCSILKAKNAGMSLGAKAAGLPSAVQWLQHQAFL 1080  
Qy 1081 KLTRHRVTVYPLLGSRTRTAQTLSEKSLPQGTTLAEEAANPALPSDFKTTILD 1132  
Db 1081 KLTRHRVTVYPLLGSRTRTAQTLSEKSLPQGTTLAEEAANPALPSDFKTTILD 1132

Query Match 100.0%; Score 5961; DB 4; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPPAPRCAVRSLSRSHYREVPLATEFVRLGSPQGNRLVQRGDPAAFRALVYQCLVCPW 60  
Db 1 MPPAPRCAVRSLSRSHYREVPLATEFVRLGSPQGNRLVQRGDPAAFRALVYQCLVCPW 60  
Qy 61 DARPPPAPPSFROVSCLKELYRVLQRLCERGAKYNLIAFGFALLDGARGGPPEAFTTSVR 120  
Db 61 DARPPPAPPSFROVSCLKELYRVLQRLCERGAKYNLIAFGFALLDGARGGPPEAFTTSVR 120  
Qy 121 SYLPLNTVTDALRGSGAWGLLRRVGDPVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLPLNTVTDALRGSGAWGLLRRVGDPVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Qy 181 ATQARPPPHASGPRRUGCERAWHNSVREAGYPLGLPAGARRGGASRSLPLPKPRR 240  
Db 181 ATQARPPPHASGPRRUGCERAWHNSVREAGYPLGLPAGARRGGASRSLPLPKPRR 240  
Qy 241 GAAPEPRTPYQGGSWAHPGRTGFDRCVVSPARPAEATSLREGALSGSTRHSHPSVG 300  
Db 241 GAAPEPRTPYQGGSWAHPGRTGFDRCVVSPARPAEATSLREGALSGSTRHSHPSVG 300  
Qy 301 RQHAGPSPTSRPPRPMDTCPCPVYBTKHLYSSSDKEQLRPSLSSLRPSLGTGARRL 360  
Db 301 RQHAGPSPTSRPPRPMDTCPCPVYBTKHLYSSSDKEQLRPSLSSLRPSLGTGARRL 360  
Qy 361 VBTIFLGSRPMPMPGTPRPLPRLPQRTWQMRPLFLLELGNHQCPYGVLLKTHCPLEAAT 420  
Db 361 VBTIFLGSRPMPMPGTPRPLPRLPQRTWQMRPLFLLELGNHQCPYGVLLKTHCPLEAAT 420  
Qy 421 PAAGWCAREKPGSVAPEEEDTDPRLVQLLROHSSPWOVYGFYRACRLRVLPGPLWGS 480  
Db 421 PAAGWCAREKPGSVAPEEEDTDPRLVQLLROHSSPWOVYGFYRACRLRVLPGPLWGS 480  
Qy 481 RHNERFRFLRNTKFKISLGKHAKLSLQELTWRMSVTDCAWLRSPGVCYPAAEHRLREEI 540  
Db 481 RHNERFRFLRNTKFKISLGKHAKLSLQELTWRMSVTDCAWLRSPGVCYPAAEHRLREEI 540

RESULT 11  
S-09-953-052-2  
Sequence 2, Application US/09953052  
Patent No. 6627619

GENERAL APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.

TITLE OF INVENTION: Antisense Compositions for Detecting and Inhibiting Telomerase Reverse Transcriptase

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/953-052  
FILING DATE: 14 Sep 2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052,919  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: US 08/844,49  
 FILING DATE: 18-APR-1997  
 APPLICATION NUMBER: US 08/846,0  
 FILING DATE: 25-APR-1997  
 APPLICATION NUMBER: US 08/851,8  
 FILING DATE: 06-MAY-1997  
 APPLICATION NUMBER: US 08/854,0  
 FILING DATE: 09-MAY-1997  
 APPLICATION NUMBER: US 08/911,3  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: US 08/912,9  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: US 08/915,5  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: US 08/974,5  
 FILING DATE: 19-NOV-1997  
 APPLICATION NUMBER: US 08/974,5  
 FILING DATE: 19-NOV-1997  
 APPLICATION NUMBER: WO PCT/US97  
 FILING DATE: 01-OCT-1997  
 APPLICATION NUMBER: WO PCT/US97  
 FILING DATE: 01-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parent, Annette S.  
 REGISTRATION NUMBER: 42,058  
 REFERENCE/DOCKET NUMBER: 015389  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 -953-052-2

ACY Match 100.0% Score 5961  
 - Local Similarity 100.0% Pred. No.  
 - Mismatch 1132; Conservative 0;  
 - Mismatches 1132;

1 MPPAPRCAVRSRSLRSHYREVPLATEVYRL  
 1 MPPAPRCAVRSRSLRSHYREVPLATEVYRL  
 61 DARPPPAFPSTQVSCRELVARYLQRLCER  
 61 DARPPPAFPSTQVSCRELVARYLQRLCER  
 121 SYLPNTVTDALRGSGAWGILRRYQGDDVLYH  
 121 SYLPNTVTDALRGSGAWGILRRYQGDDVLYH  
 61 ATQARPPPHASGPRRLGCERAWNHSVREAG  
 61 ATQARPPPHASGPRRLGCERAWNHSVREAG  
 121 SYLPNTVTDALRGSGAWGILRRYQGDDVLYH  
 121 SYLPNTVTDALRGSGAWGILRRYQGDDVLYH  
 181 ATQARPPPHASGPRRLGCERAWNHSVREAG  
 181 ATQARPPPHASGPRRLGCERAWNHSVREAG  
 241 GAAPEPERTPGQGSWAHGPTRQPSDRGFC  
 241 GAAPEPERTPGQGSWAHGPTRQPSDRGFC  
 301 RQHAGGPPSTSRRPWPDTCPYPAETKHF  
 301 RQHAGGPPSTSRRPWPDTCPYPAETKHF  
 361 VETIFLGSRPMMGCTPRLPRLPQRYWQMRP  
 361 VETIFLGSRPMMGCTPRLPRLPQRYWQMRP  
 421 PAAGVCAERPKQGSVAAPEBETDPRRLVQL

RESULTS 12

US-09-042-460-3

1 Sequence 3, Application US/09042460

1 Patent No. 6767719

1 GENERAL INFORMATION

1 APPLICANT: Morin, Gregg B.

1 APPLICANT: Allsopp, Richard

1 APPLICANT: DePinho, Ronald

1 APPLICANT: Greenberg, Roger

1 TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase

1 NUMBER OF SEQUENCES: 101

1 CORRESPONDENCE ADDRESS:

1 ADDRESS: Townsend and Townsend and Crew LLP

1 STREET: Two Embarcadero Center, Eighth Floor

1 CITY: San Francisco

1 STATE: California

1 COUNTRY: USA

1 ZIP: 94111-3834

1 MEDIUM TYPE: Floppy disk

1 COMPUTER: IBM PC compatible

1 OPERATING SYSTEM: PC-DOS/MS-DOS

1 SOFTWARE: Patent in Release #1.0, Version #1.30

1 CURRENT APPLICATION DATA:

1 APPLICATION NUMBER: US/09/042,460

1 Query Match 100.0% Score 5961; D

1 Best Local Similarity 100.0% Pred. No. 0;

1 Matches 1132; Conservative 0; Missmatches 0

1 FILING DATE: 16-MAR-1998

1 CLASSIFICATION: 536

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: US 08/724,643

1 FILING DATE: 01-OCT-1996

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: US 08/844,419

1 FILING DATE: 18-APR-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: US 08/846,017

1 FILING DATE: 25-APR-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: US 08/851,843

1 FILING DATE: 06-MAY-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: US 08/854,050

1 FILING DATE: 09-MAY-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: US 08/911,312

1 FILING DATE: 14-AUG-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: US 08/912,951

1 FILING DATE: 14-AUG-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: WO PCT/US97/17618

1 FILING DATE: 01-OCT-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: WO PCT/US97/17885

1 FILING DATE: 14-AUG-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: WO PCT/US97/17885

1 FILING DATE: 01-OCT-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: US 08/915,503

1 FILING DATE: 14-AUG-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: US 08/915,503

1 FILING DATE: 01-OCT-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: WO PCT/US97/17618

1 FILING DATE: 01-OCT-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: WO PCT/US97/17885

1 FILING DATE: 01-OCT-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: US 08/974,549

1 FILING DATE: 19-NOV-1997

1 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER: US 08/974,549

1 FILING DATE: 19-NOV-1997

1 ATTORNEY/AGENT INFORMATION:

1 NAME: Einhorn, Gregory P.

1 REGISTRATION NUMBER: 38,440

1 REFERENCE/DOCKET NUMBER: 015389-003110US

1 TELECOMMUNICATION INFORMATION:

1 TELEPHONE: (415) 576-0200

1 TELEFAX: (415) 576-0300

1 INFORMATION FOR SEQ ID NO: 3:

1 SEQUENCE CHARACTERISTICS:

1 LENGTH: 1132 amino acids

1 TYPE: amino acid

1 STANDINGNESS:

1 TOPOLOGY: linear

1 MOLECULE TYPE: protein

1 FEATURE:

1 NAME/KEY: protein

1 LOCATION: 1..1132

1 OTHER INFORMATION: /note= "human telomerase (hTRT)"

1 US-09-042-460-3

QY 121 SYLPNTVTDALRGSGAWGLLRLRRVGDVLVHLARCAFLVLA  
Db 121 SYLPNTVTDALRGSGAWGLLRLRRVGDVLVHLARCAFLVLA  
QY 181 ATQARPPPHASPRERLGCERAWHNSVREAGVPLGPAPGARRGGASRSRSLPLPKRPRR 240  
Db 181 ATQARPPPHASPRERLGCERAWHNSVREAGVPLGPAPGARRGGASRSRSLPLPKRPRR 240  
QY 241 GAAPPERTRPQGGSWAHPGTRGSRSRSLPLPKRPRR 300  
Db 241 GAAPPERTRPQGGSWAHPGTRGSRSRSLPLPKRPRR 300  
QY 301 RQHHACPPSTSRSRPPRWDTCPCPVYAAETKHFLYSSGCKEQLRPSFLLSSRLRSLTGARRL 360  
Db 301 RQHHACPPSTSRSRPPRWDTCPCPVYAAETKHFLYSSGCKEQLRPSFLLSSRLRSLTGARRL 360  
QY 361 VETIFLGSRPPMPGTFRPLPPLPQRYWQMPPLFELLGNAHQCPYGVLLKTHCPRAVAT 420  
Db 361 VETIFLGSRPPMPGTFRPLPPLPQRYWQMPPLFELLGNAHQCPYGVLLKTHCPRAVAT 420  
QY 421 PAAGYCAREXPGSYAAPEEEDTDPRLVQLLROISSPQVYGFTRACLRLVPGFLWGS 480  
Db 421 PAAGYCAREXPGSYAAPEEEDTDPRLVQLLROISSPQVYGFTRACLRLVPGFLWGS 480  
QY 481 RHNERRFLRNTKKFISLGKETAKLSQLBLTWMKSRDCAWLRSPGVYCUPAAEHLREII 540  
Db 481 RHNERRFLRNTKKFISLGKETAKLSQLBLTWMKSRDCAWLRSPGVYCUPAAEHLREII 540  
QY 541 LAKFLIWLMSVYVLLRSFFYVTTETFQKNRLLFYRKSYWSKLSQIGIRQLKRVOLRE 600  
Db 541 LAKFLIWLMSVYVLLRSFFYVTTETFQKNRLLFYRKSYWSKLSQIGIRQLKRVOLRE 600  
QY 601 LSEAEVRLQHREARPALITSRFLPKPDRIPVNNMDYVGARTPREKRAERLTSRVRKA 660  
Db 601 LSEAEVRLQHREARPALITSRFLPKPDRIPVNNMDYVGARTPREKRAERLTSRVRKA 660  
QY 661 LFSVNLNEYERARRPGLGASVGLDDTHRAWTFVLRQAQDPPLFYKVDTGAYDTI 720  
Db 661 LFSVNLNEYERARRPGLGASVGLDDTHRAWTFVLRQAQDPPLFYKVDTGAYDTI 720  
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Db 781 QETSPRDAVYIEQSSSLNEASGIFDVFERFMCHAVRTRGKSTVQCGQIPQGSILSTL 840  
QY 841 LCLSLCYGDMEKLFACIRRDCLLRLYDDFLVTPHILTHAKTFLATLVRGVPYEGCVNL 900  
Db 841 LCLSLCYGDMEKLFACIRRDCLLRLYDDFLVTPHILTHAKTFLATLVRGVPYEGCVNL 900  
QY 901 RKTIVNFPVDEALGTAFYOMPAHGLFPWCGLLDRTTLEQSDYSSTARTSTRASLTF 960  
Db 901 RKTIVNFPVDEALGTAFYOMPAHGLFPWCGLLDRTTLEQSDYSSTARTSTRASLTF 960  
QY 961 NRGFXKGRNMRKLFACIRRDCLLRLYDDFLVTPHILTHAKTFLATLVRGVPYEGCVNL 1020  
Db 961 NRGFXKGRNMRKLFACIRRDCLLRLYDDFLVTPHILTHAKTFLATLVRGVPYEGCVNL 1020  
QY 1021 FHQQWKNPKTFLRVISDTASLCYSTIKAKAGMISLGAKGAAGPLPSEAVQLCHQAFLL 1080  
Db 1021 FHQQWKNPKTFLRVISDTASLCYSTIKAKAGMISLGAKGAAGPLPSEAVQLCHQAFLL 1080  
QY 1081 KLTRHRVTVYPLGSLRSTAQTQLSRKLPGTTLTALEAANPALSDFKTLID 1132  
Db 1081 KLTRHRVTVYPLGSLRSTAQTQLSRKLPGTTLTALEAANPALSDFKTLID 1132

Patent No. 6166178  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/917,1618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/917,17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 0153389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
SEQUENCE CHARACTERISTICS: 611:  
LENGTH: 1154 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein

LOCATION: 1..1154 OTHER INFORMATION: /note= "fusion protein composed of htrt protein sequence, vector sequences, the Myc epitope and His6 tag" OTHER INFORMATION: Myc epitope and His6 tag" US-08-974-59A-611

Query Match 100.0%; Score 5961; DB 3; Length 1154;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MPRAPRCAVRSILSRSHREREVPLATEVRRGPGQWVQGDPAARALVAQCLVCVPW 60  
1 MPRAPRCAVRSILSRSHREREVPLATEVRRGPGQWVQGDPAARALVAQCLVCVPW 60

61 DARPPAPSPFQVSCRELAYRVLQRLCERGAKNVLAFGFLALDQARGGPEAFTTSVR 120  
61 DARPPAPSPFQVSCRELAYRVLQRLCERGAKNVLAFGFLALDQARGGPEAFTTSVR 120

121 SYLPNTVTDALRGSGAWGLLRRGGDVLVHLLARCAFLVAPSCAYQVCGPPLYQLG 180  
121 SYLPNTVTDALRGSGAWGLLRRGGDVLVHLLARCAFLVAPSCAYQVCGPPLYQLG 180

181 ATQARPPPHASGPRRRLGGERAWNNSVREACVPLGPAPGARRGGSARSLSLPKPRPR 240  
181 ATQARPPPHASGPRRRLGGERAWNNSVREACVPLGPAPGARRGGSARSLSLPKPRPR 240

241 GRAPEPERTPYGGSGWAHPGTRGPDRGFCVSPARABEATSLEGALSGRTRSHPSVG 300  
241 GRAPEPERTPYGGSGWAHPGTRGPDRGFCVSPARABEATSLEGALSGRTRSHPSVG 300

301 RQHAGFPSTSRPSPWDTPCPPTVAAETKHFLYSSGDKEDOLRSPFSLSSURPSLGTARRL 360  
301 RQHAGFPSTSRPSPWDTPCPPTVAAETKHFLYSSGDKEDOLRSPFSLSSURPSLGTARRL 360

361 VETIFLGSRPMPGTPRPLPPLPQRYWQMPRLPFLLELLGNAHQACPYGVLLKTHCPLRAVT 420  
361 VETIFLGSRPMPGTPRPLPPLPQRYWQMPRLPFLLELLGNAHQACPYGVLLKTHCPLRAVT 420

421 PAAGVCAREKQGSVAAPEEDTDRRLQJLRRQHSSPQVYGVPRACJRRLYVPGLGWS 480  
421 PAAGVCAREKQGSVAAPEEDTDRRLQJLRRQHSSPQVYGVPRACJRRLYVPGLGWS 480

421 PAAGVCAREKQGSVAAPEEDTDRRLQJLRRQHSSPQVYGVPRACJRRLYVPGLGWS 480

481 RHNERFLRNTKTFPSLGHAKLSQLQELTWKMSYRDCANLRRSPGVGCPAAEHLRREI 540  
481 RHNERFLRNTKTFPSLGHAKLSQLQELTWKMSYRDCANLRRSPGVGCPAAEHLRREI 540

541 LSEAEVRLQRREARPALLTSRLRFIPKPGDSHARPITNMDDVYGAETFRRKRAEFLTSRKVA 660  
541 LSEAEVRLQRREARPALLTSRLRFIPKPGDSHARPITNMDDVYGAETFRRKRAEFLTSRKVA 660

601 LSEAEVRLQRREARPALLTSRLRFIPKPGDSHARPITNMDDVYGAETFRRKRAEFLTSRKVA 660  
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601 LSEAEVRLQRREARPALLTSRLRFIPKPGDSHARPITNMDDVYGAETFRRKRAEFLTSRKVA 660

661 LPSVLYNERARRPGILGASVYLGLDIHRAWTRFVLRVAQDPPELYVVKVDVTGAYDTI 720  
661 LPSVLYNERARRPGILGASVYLGLDIHRAWTRFVLRVAQDPPELYVVKVDVTGAYDTI 720

721 PQDRLTEVIASTIKPQNTYCVRRYAVVOKAAGHGVRAFKSHVSTLTLQPYMROFV AHL 760  
721 PQDRLTEVIASTIKPQNTYCVRRYAVVOKAAGHGVRAFKSHVSTLTLQPYMROFV AHL 780

781 QETSPRLDAVVIQOSSSNEAASSGLFDPYELRFENCHAVRIGKSYVQCGIPOGSILSTI 840  
781 QETSPRLDAVVIQOSSSNEAASSGLFDPYELRFENCHAVRIGKSYVQCGIPOGSILSTI 840

841 LCSIQYGMENKLFAGIIRRDGLLRLVDDFLYVPLTHAKTFLRLVGVPEYGCVNL 900  
841 LCSIQYGMENKLFAGIIRRDGLLRLVDDFLYVPLTHAKTFLRLVGVPEYGCVNL 900

901 RKTIVNPFYVEDAEGTAVQMPAHGLPPWCGIILDTTRLEYQSDYSSYARTSIRASLT F 960  
901 RKTIVNPFYVEDAEGTAVQMPAHGLPPWCGIILDTTRLEYQSDYSSYARTSIRASLT F 960

Db Qy 961 NRGFKAGRNMRRKLFQGVLRKCHSILFLQVNISIQTVCNTNIKILLQAYRFHACVVLQLP 1020  
Db Qy 961 NRGFKAGRNMRRKLFQGVLRKCHSILFLQVNISIQTVCNTNIKILLQAYRFHACVVLQLP 1020

Db Qy 961 NRGFKAGRNMRRKLFQGVLRKCHSILFLQVNISIQTVCNTNIKILLQAYRFHACVVLQLP 1080  
Db Qy 1021 FHQQWKNPTEFLVVISDASLCVSLKAKNAGMSLGAAGAFLPSEAVQWLCQHQAFL 1080  
Db Qy 1021 FHQQWKNPTEFLVVISDASLCVSLKAKNAGMSLGAAGAFLPSEAVQWLCQHQAFL 1080

Db Qy 1081 KLTHRHRTVPLIGSLRTAQTLQSLRKPCTTLTALEAANPAPLPSDFKTLID 1132  
Db Qy 1081 KLTHRHRTVPLIGSLRTAQTLQSLRKPCTTLTALEAANPAPLPSDFKTLID 1132

Db Qy 1081 KLTHRHRTVPLIGSLRTAQTLQSLRKPCTTLTALEAANPAPLPSDFKTLID 1132

Db Qy 1081 KLTHRHRTVPLIGSLRTAQTLQSLRKPCTTLTALEAANPAPLPSDFKTLID 1132

RESULT 14  
US-08-912-951-323  
Sequence 323, Application US/08912951  
; Patent No. 6475789  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R,  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,951  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,543  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002600US  
; TELECOMMUNICATION: (415) 576-0200  
; TELEFAX: (415) 576-0100  
; INFORMATION FOR SEQ ID NO: 323:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1154 amino acids  
 TYPE: amino acid

STRANDEDNESS:  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-912-951-323

Query Match 100.0%; Score 5961; DB 4; Length 1154;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Gaps 0;

Db 901 RKTIVNPFVDEALGGTAFQMPAHGLFPWCGLLDTRLEQSDYSSYARTSIRASLT 960  
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 Db 961 NRGFAGGRNRRKFLGVLKUCHSFLDQVNSLQTVCTNLYKJLQLQTRFHACTVQLP 1020  
 Qy 1021 FHQQWKNPTEFLRIVTSDTASLCSILKAKNAGMSLGAKGAAGLPLSEAVOWLCHOAFL 1080  
 Db 1021 FHQQWKNPTEFLRIVTSDTASLCSILKAKNAGMSLGAKGAAGLPLSEAVOWLCHOAFL 1080  
 Qy 1081 KLTTRHRTVYPLLSLRTAQTQLSRKLPGTTLALEAAANPALPSDFKTLID 1132  
 Db 1081 KLTTRHRTVYPLLSLRTAQTQLSRKLPGTTLALEAAANPALPSDFKTLID 1132

RESULT 15  
 US-09-402-181B-611  
 Sequence 611, Application US/09402181B  
 Patent No. 6610839  
 GENERAL INFORMATION:  
 APPLICANT: Cech, Thomas R. ✓  
 Lingner, Joachim  
 Nakamura, Toru  
 Chapman, Karen B.  
 Morin, Gregg B.  
 Harley, Calvin B.  
 Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
 NUMBER OF SEQUENCES: 633  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/402,181B  
 FILING DATE: 23-Sep-1997  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/724,643  
 FILING DATE: 01-OCT-1996  
 APPLICATION NUMBER: US 08/844,419  
 FILING DATE: 18-APR-1997  
 APPLICATION NUMBER: US 08/846,017  
 FILING DATE: 25-APR-1997  
 APPLICATION NUMBER: US 08/851,843  
 FILING DATE: 06-MAY-1997  
 APPLICATION NUMBER: US 08/854,050  
 FILING DATE: 09-MAY-1997  
 APPLICATION NUMBER: US 08/911,312  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: US 08/912,951  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: US 08/915,503  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: WO PCT/US97/17885  
 FILING DATE: 01-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ausenhub, Scott L.  
 REGISTRATION NUMBER: 42  
 REFERENCE/DOCKET NUMBER: 015389-002620US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 611:

Db 901 RKTIVNPFVDEALGGTAFQMPAHGLFPWCGLLDTRLEQSDYSSYARTSIRASLT 960  
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 Db 961 NRGFAGGRNRRKFLGVLKUCHSFLDQVNSLQTVCTNLYKJLQLQTRFHACTVQLP 1020  
 Qy 1021 FHQQWKNPTEFLRIVTSDTASLCSILKAKNAGMSLGAKGAAGLPLSEAVOWLCHOAFL 1080  
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 Qy 1081 KLTTRHRTVYPLLSLRTAQTQLSRKLPGTTLALEAAANPALPSDFKTLID 1132  
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Db 1121 SYLPNTVTDALRGSGAWGLLRLRGGDDVLVHLARCAFLVAPSCAYQVCGPLYQLGA 180  
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 Qy 181 ATQARPYPHASGPRRLGCERAWNHSVREACVPLGAPGARRGGSASSLPLPKRPRR 240  
 Db 181 ATQARPYPHASGPRRLGCERAWNHSVREACVPLGAPGARRGGSASSLPLPKRPRR 240  
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 Qy 361 VETIFLGSRPNMPGTPRPLPRLPQRYWQMRPLFELLGNAHQCPYGVLLKTHCPLRAVFT 420  
 Db 361 VETIFLGSRPNMPGTPRPLPRLPQRYWQMRPLFELLGNAHQCPYGVLLKTHCPLRAVFT 420  
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 Db 421 PAAGVCAREKPKGSVAAPEEEDTDPRLVQLLROHSSPWWQVQGYFVRACLRLVPGFLWGS 480  
 Qy 481 RHNERFLRNTYKFKISLGKHAKLSQLELTWKMSVRDCAWLRSPGVGCPAAEHLRREI 540  
 Db 481 RHNERFLRNTYKFKISLGKHAKLSQLELTWKMSVRDCAWLRSPGVGCPAAEHLRREI 540  
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 Db 841 LCSLCYGDMEKFLAGTRDCELLRIVDDFLVTPH THATFLTFLVQGVPEYCCVNL 900  
 Qy 901 RKTIVNPFVDEALGGTAFQMPAHGLFPWCGLLDTRLEQSDYSSYARTSIRASLT 960

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1154 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <unknown>  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..1154  
 OTHER INFORMATION: /note= "fusion protein composed of hrt  
 protein sequence, vector sequences, the  
 Myc epitope and His6 tag"  
 SEQUENCE DESCRIPTION: SEQ ID NO: 611:  
 US-09-402-181B-611

Query Match 100.0%; Score 5961; DB 4; Length 1154;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPPAPRCAVRSLRSHYREVPLATVRRQGPQWMLVQRGDPAAFLVAQCLVCPW 60  
 Db 1 MPPAPRCAVRSLRSHYREVPLATVRRQGPQWMLVQRGDPAAFLVAQCLVCPW 60

Qy 61 DARPPPAAPSPQQVSKELVQLCBERGAKVNLAFGFLALDARGGPEAFTTSVR  
 Db 61 DARPPPAAPSPQQVSKELVQLCBERGAKVNLAFGFLALDARGGPEAFTTSVR

Qy 121 SYPNTVTDALRGSGAWLLRVRGDDVLVHLLARCAFLVAPCAYQVCGPPLYQJGA 180  
 Db 121 SYPNTVTDALRGSGAWLLRVRGDDVLVHLLARCAFLVAPCAYQVCGPPLYQJGA 180

Qy 181 ATQARPPhASGPRRLGCBDAWNSVREAGVPLGPAGARRGGSaRSLLPKRPR 240  
 Db 181 ATQARPPhASGPRRLGCBDAWNSVREAGVPLGPAGARRGGSaRSLLPKRPR 240

Qy 241 GAAPEPRTPYQGQSAHPGTRGSDRGFCVVSAPAAEATSLGALSGTRHSHPSVG 300  
 Db 241 GAAPEPRTPYQGQSAHPGTRGSDRGFCVVSAPAAEATSLGALSGTRHSHPSVG 300

Qy 301 RQHHAGPSTSRRPPRWDTCPPTVIAETRFLYSSGDEQLRPFLLSSRLPPLKRR 360  
 Db 301 RQHHAGPSTSRRPPRWDTCPPTVIAETRFLYSSGDEQLRPFLLSSRLPPLKRR 360

Qy 361 VETIFGSRPMPGTPRLPRLPQYQWMPRLPFLLEQHNAQCPYGVJLKHGSPIRAVT 420  
 Db 361 VETIFGSRPMPGTPRLPRLPQYQWMPRLPFLLEQHNAQCPYGVJLKHGSPIRAVT 420

Qy 421 PAAGTCAREKPGQSTAAPEEEDTDPRLVYQQLRHOHSSPQVQYGFVRAQLRVPQGMS 480  
 Db 421 PAAGTCAREKPGQSTAAPEEEDTDPRLVYQQLRHOHSSPQVQYGFVRAQLRVPQGMS 480

Qy 481 RHNERRFLRNTKTKTSIGKHAKSLSQELTWKMSYRDCAWLRRSPGVGVPAEHRREI 540  
 Db 481 RHNERRFLRNTKTKTSIGKHAKSLSQELTWKMSYRDCAWLRRSPGVGVPAEHRREI 540

Qy 541 LAKFTHWLMNSVYVYELLRFYYTTTQNRLEFYRKSWSKLSIGTROHLKRYLRE 600  
 Db 541 LAKFTHWLMNSVYVYELLRFYYTTTQNRLEFYRKSWSKLSIGTROHLKRYLRE 600

Qy 601 LSEAEVRQREARPAALLTSRLRFKPKPGLRPIVNMDYVVGARTFRIEKRERLTSRVA 660  
 Db 601 LSEAEVRQREARPAALLTSRLRFKPKPGLRPIVNMDYVVGARTFRIEKRERLTSRVA 660

Qy 661 LFSVLYNERYARRPGLLGSVGLDDIHRMWRTEVLVRAQDPPPELYFVYKDVTDYDTI 720  
 Db 661 LFSVLYNERYARRPGLLGSVGLDDIHRMWRTEVLVRAQDPPPELYFVYKDVTDYDTI 720

Qy 721 PQDRLTEVIASTIKPQNTYCYRRAVYQKAAGHVKFKSHVSTLTDQYMRQFVHL 780  
 Db 721 PQDRLTEVIASTIKPQNTYCYRRAVYQKAAGHVKFKSHVSTLTDQYMRQFVHL 780

Qy 781 QETSPRLDAVVIQSSSNEASSGLPDFVLRFMCHHAVRGKSYVQCQGIPQGSTLSTL 840